FIG. 1A

```
    ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTTCCCCAGCTGCCCGGCTGCTGC
1   ---------+---------+---------+---------+---------+---------+
    TACACCTTTACCTATGACTGTGTAACACGGAGTCGGAAAGGGGTGGACGGGCCGACGACG   60

     M  W  K  W  I  L  T  H  C  A  S  A  F  P  H  L  P  G  C  C  -

    TGCTGCTGCTTTTTGTTGCTGTTCTTGGTGTCTTCCGTCCCTGTCACCTGCCAAGCCCTT
61  ---------+---------+---------+---------+---------+---------+
    ACGACGACGAAAAACAACGACAAGAACCACAGAAGGCAGGGACAGTGGACGGTTCGGGAA   120

     C  C  C  F  L  L  L  F  L  V  S  S  V  P  V  T  C  Q  A  L  -

    GGTCAGGACATGGTGTCACCAGAGGCCACCAACTCTTCTTCCTCCTCCTTCTCCTCTCCT
121 ---------+---------+---------+---------+---------+---------+
    CCAGTCCTGTACCACAGTGGTCTCCGGTGGTTGAGAAGAAGGAGGAGGAAGAGGAGAGGA   180

     G  Q  D  M  V  S  P  E  A  T  N  S  S  S  S  S  F  S  S  P  -

    TCCAGCGCGGGAAGGCATGTgCGGAGCTACAATCACCTTCAAGGAGATGTCCGCTGGAGA
181 ---------+---------+---------+---------+---------+---------+
    AGGTCGCGCCCTTCCGTACAcGCCTCGATGTTAGTGGAAGTTCCTCTACAGGCGACCTCT   240

     S  S  A  G  R  H  V  R  S  Y  N  H  L  Q  G  D  V  R  W  R  -
```

MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

FIG. 1B

```
    AAGCTATTCTCTTTCACCAAGTACTTTCTCAAGATTGAGAAGAACGGGAAGGTCAGCGGG
241 ---------+---------+---------+---------+---------+---------+ 300
    TTCGATAAGAGAAAGTGGTTCATGAAAGAGTTCTAACTCTTCTTGCCCTTCCAGTCGCCC

     K  L  F  S  F  T  K  Y  F  L  K  I  E  K  N  G  K  V  S  G  -

    ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT
301 ---------+---------+---------+---------+---------+---------+ 360
    TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAA

     T  K  K  E  N  C  P  Y  S  I  L  E  I  T  S  V  E  I  G  V  -

    GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC
361 ---------+---------+---------+---------+---------+---------+ 420
    CAACGGCAGTTTCGGTAATTGTCGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAG

     V  A  V  K  A  I  N  S  N  Y  Y  L  A  M  N  K  K  G  K  L  -

    TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA
421 ---------+---------+---------+---------+---------+---------+ 480
    ATACCGAGTTTTCTTAAATTGTTACTGACATTCGACTTCCTCTCCTATCTCCTTTTACCT

     Y  G  S  K  E  F  N  N  D  C  K  L  K  E  R  I  E  E  N  G  -
```

MATCH WITH FIG. 1C

MATCH WITH FIG. 1B **FIG. 1C**

```
     TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG
481  ---------+---------+---------+---------+---------+---------+ 540
     ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCCGTTTACATACACCGTAAC

      Y  N  T  Y  A  S  F  N  W  Q  H  N  G  R  Q  M  Y  V  A  L  -

     AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC
541  ---------+---------+---------+---------+---------+---------+ 600
     TTACCTTTTCCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGAGACGAGTG

      N  G  K  G  A  P  R  R  G  Q  K  T  R  R  K  N  T  S  A  H  -

     TTTCTTCCAATGGTGGTACACTCATAG
601  ---------+---------+------- 627
     AAAGAAGGTTACCACCATGTGAGTATC
      F  L  P  M  V  V  H  S  *
```

FIG. 2A

```
      1                                                          50
FGF4  MS.GPGTAAV ALLPAVLLAL LA........ .PWAGRGGAA APTAPNGTLE
FGF6  MSRGAGRLQG TLWALVFLGI LV........ .GMVVPSPAG TR.ANNTLLD
FGF5  .......MSL SFLLLLFFSH LILSAWAHGE KRLAPKGQPG PAATDRNPIG
FGF1  .......... .......... .......... .......... ..........
FGF2  .......... .......... .......... .......... ..........
FGF9  .......... .......... .......... .......... ..........
FGF7  .......... ......MHKW ILTWILPTLL ..MAPLGEVG NYFGVQDAVP
KGF2  .......... ......MWKW ILTHCASAFP .....YRSCF HIICLVGTIS
FGF3  .......... .......... .......... HLPGCCCCCF LLLFLVSSVP
FGF8  MGSPRSALSC LLLHLLVLCL QAQVRSAAQK .......MGL IWLLLLSLLE
                                       RGPGAGNPAD TLGQGHEDRP

      51                                                         100
FGF4  AELERRWESL VALSLARLPV AA..QPKEAA VQSGAGDY.. ...LLGIKRL
FGF6  S...RGWGTL LSRSRAGLAG EI......AG VNWESG.Y.. ...LVGIKRQ
FGF5  SSSRQSSSSA MSSSSASSSP AASLGSQGSG LEQSSFQW.. ...SPSGRRT
FGF1  ......MAEG EITTFTALTE KFN...LPPG .......N.. ...YK...KP
FGF2  ......MAAG SITTLPALPE DGGSGAFPPG .......H.. ...FK...DP
FGF9  FGNVPVLPVD SPVLLSDHLG QSEAGGLPRG PAVTDLDH.. ...LKGILRR
FGF7  LACNDMTPEQ M...ATNVNC ......SSPE RHTRSYDY.. ...MEGGDIR
KGF2  VTCQALGQDM VSPEATNSSS SSFSSPSSAG RHVRSYNH.. ...LQ.GDVR
FGF3  PGWPAAGPGA .......... ...RLRRDAG GRGGVYEH.. ...L.GGAPR
FGF8  FGQRSRAGKN FTNPAPNYPE EGSKEQRDSV LPKVTQRHVR EQSLVTDQLS
```

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

FIG. 2B

```
     101                                                    150
FGF4 RRL.....YC NVGIGFHLQA LPDGRIGGAH ADT.RDSLLE LSPVERGV.V
FGF6 RRL.....YC NVGIGFHLQV LPDGRISGTH EEN.PYSLLE ISTVERGV.V
FGF5 GSL.....YC RVGIGFHLQI YPDGKVNGSH EAN.MLSVLE IFAVSQGI.V
FGF1 KLL.....YC SNG.GHFLRI LPDGTVDGTR DRSDQHIQLQ LSAESVGE.V
FGF2 KRL.....YC KNG.GFFLRI HPDGRVDGVR EKSDPHIKLQ LQAEERGV.V
FGF9 RQL.....YC R.T.GFHLEI FPNGTIQGTR KDHSRFGILE FISIAVGL.V
FGF7 VRR.....LF CRT.QWYLRI DKRGKVKGTQ EMKNNYNIME IRTVAVGI.V
KGF2 WRK.....LF SFT.KYFLKI EKNGKVSGTK KENCPYSILE ITSVEIGV.V
FGF3 RRK.....LY CAT.KYHLQL HPSGRVNGSL .ENSAYSILE ITAVEVGI.V
FGF8 RRLIRTYQLY SRTSGKHVQV LANKRINAMA EDGDPFAKLI VETDTFGSRV

     151                                                    200
FGF4 SIFGVASRFF VAMSSKGKLY G.SPFFTDEC TFKEILLPNN YNAYESYKYP
FGF6 SLFGVRSALF VAMNSKGRLY A.TPSFQEEC KFRETLLPNN YNAYESDLYQ
FGF5 GIRGVFSNKF LAMSKKGKLH A.SAKFTDDC KFRERFQENS YNTYASAIHR
FGF1 YIKSTETGQY LAMDTDGLLY G.SQTPNEEC LFLERLEENH YNTYISKKH.
FGF2 SIKGVCANRY LAMKEDGRLL A.SKCVTDEC FFFERLESNN YNTYRSRKY.
FGF9 SIRGVDSGLY LGMNEKGELY G.SEKLTQEC VFREQFEENW YNTYSSNLYK
FGF7 AIKGVESEFY LAMNKEGKLY A.KKECNEDC NFKELILENH YNTYAS....
KGF2 AVKAINSNYY LAMNKKGKLY G.SKEFNNDC KLKERIEENG YNTYAS....
FGF3 AIRGLFSGRY LAMNKRGRLY A.SEHYSAEC EFVERIHELG YNTYASRLYR
FGF8 RVRGAETGLY ICMNKKGKLI AKSNGKGKDC VFTEIVLENN YTALQNAKY.
```

MATCH WITH FIG. 2C

MATCH WITH FIG. 2B

FIG. 2C

```
      201                                                         250
FGF4  ..........  GM......FI  ALSKNGKTKK  G..NRVSPTM  KVTHFLPRL.
FGF6  ..........  GT......YI  ALSKYGRVKR  G..SKVSPIM  TVTHFLPRI.
FGF5  ..........  TEKTGREWYV  ALNKRGKAKR  GCSPRVKPQH  ISTHFLPRFK
FGF1  ..........  ...AEKNWFV  GLKKNGSCKR  G..PRTHYGQ  KAILFLPLPV
FGF2  ..........  ...T..SWYV  ALKRTGQYKL  G..SKTGPGQ  KAILFLPMSA
FGF9  HV........  ..DTGRRYYV  ALNKDGTPRE  G..TRTKRHQ  KFTHFLPRPV
FGF7  .......AKW  THNGGEM.FV  ALNQKGIPVR  G..KKTKKEQ  KTAHFLPMAI
KGF2  .......FNW  QHNGRQM.YV  ALNGKGAPRR  G..QKTRRKN  TSAHFLPMVV
FGF3  TVSSTPGARR  QPSAERLWYV  SVNGKGRPRR  G..FKTRRTQ  KSSLFLPRVL
FGF8  ..........  .....EGWYM  AFTRKGRPRK  G..SKTRQHQ  REVHFMKRLP

      251                                                         300
FGF4  ..........  ..........  ..........  ..........  ..........
FGF6  ..........  ..........  ..........  ..........  ..........
FGF5  QSEQPELSFT  VTVPEKKNPP  SPIKSKIPLS  ..........  ..........
FGF1  SSD.......  ..........  ..........  APRKNTNSVK  YRLKFRFG..
FGF2  KS........  ..........  ..........  ..........  ..........
FGF9  DPDKVPELYK  DILSQS....  ..........  ..........  ..........
FGF7  T.........  ..........  ..........  ..........  ..........
KGF2  HS........  ..........  ..........  ..........  ..........
FGF3  DHRDHEMVRQ  LQSGLPRPPG  KGVQPRRRRQ  KQSPDNLEPS  HVQASRLGSQ
FGF8  RGHHTTEQSL  RFEFLNYPPF  TRSLRGSQRT  WAPEPR....  ..........
```

MATCH WITH FIG. 2D

MATCH WITH FIG. 2C

FIG. 2D

	301
FGF4	......
FGF6	......
FGF5	......
FGF1	......
FGF2	......
FGF9	......
FGF7	......
KGF2	......
FGF3	LEASAH
FGF8	......

Figure 3A

```
GGAATTCCGG GAAGAGAGGG AAGAAAACAA CGGCGACTGG GCAGCTGCCT CCACTTCTGA     60
CAACTCCAAA GGGATATACT TGTAGAAGTG GCTCGCAGGC TGGGGCTCCG CAGAGAGAGA    120
CCAGAAGGTG CCAACCGCAG AGGGGTGCAG ATATCTCCCC CTATTCCCCA CCCCACCTCC    180
CTTGGGTTTT GTTCACCGTG CTGTCATCTG TTTTTCAGAC CTTTTTGGCA TCTAACATGG    240
TGAAGAAAGG AGTAAAGAAG AGAACAAAGT AACTCCTGGG GGAGCGAAGA GCGCTGGTGA    300
CCAACACCAC CAACGCCACC ACCAGCTCCT GCTGCTGCGG CCACCCACGT CCACCATTTA    360
CCGGGAGGCT CCAGAGGCGT AGGCAGCGGA TCCGAGAAAG GAGCGAGGGG AGTCAGCCGG    420
CTTTTCCGAG GAGTTATGGA TGTTGGTGCA TTCACTTCTG GCCAGATCCG CGCCCAGAGG    480
GAGCTAACCA GCAGCCACCA CCTCGAGCTC TCTCCTTGCC TTGCATCGGG TCTTACCCTT    540
CCAGTATGTT CCTTCTGATG AGACAATTTC CAGTGCCGAG AGTTTCAGTA CA ATG        595
                                                           Met

TGG AAA TGG ATA CTG ACA CAT TGT GCC TCA GCC TTT CCC CAC CTG CCC      643
Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro

GGC TGC TGC TGC TGC TGC TTT TTG TTG CTG TTC TTG GTG TCT TCC GTC      691
Gly Cys Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val

CCT GTC ACC TGC CAA GCC CTT GGT CAG GAC ATG GTG TCA CCA GAG GCC      739
Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala

ACC AAC TCT TCT TCC TCC TCC TTC TCC TCT CCT TCC AGC GCG GGA AGG      787
Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg

CAT GTG CGG AGC TAC AAT CAC CTT CAA GGA GAT GTC CGC TGG AGA AAG      835
His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg Lys

CTA TTC TCT TTC ACC AAG TAC TTT CTC AAG ATT GAG AAG AAC GGG AAG      883
Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys

GTC AGC GGG ACC AAG AAG GAG AAC TGC CCG TAC AGC ATC CTG GAG ATA      931
Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile

ACA TCA GTA GAA ATC GGA GTT GTT GCC GTC AAA GCC ATT AAC AGC AAC      979
Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn

TAT TAC TTA GCC ATG AAC AAG AAG GGG AAA CTC TAT GGC TCA AAA GAA     1027
Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu

TTT AAC AAT GAC TGT AAG CTG AAG GAG AGG ATA GAG GAA AAT GGA TAC     1075
Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly Tyr
```

Figure 3B

AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT 1123
Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr

GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA 1171
Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg

AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA 1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser

TAGAGGAAGG CAACGTTTGT GGATGCAGTA AAACCAATGG CTCTTTTGCC AAGAATAGTG 1276

GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC 1336

TTAAAAGAAA GCCAGCCTTT GAAGGTTTTT GTATTCACTG CTGACATATG ATGTTCTTTT 1396

AATTAGTTCT GTGTCATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT 1456

ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTTGTTGT TGTTGTCAAG TTTTTGTTTT 1516

TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAATCT GTTGAAAGAA CGATCTTCGG 1576

GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT 1636

GAATCAATGA ACAGTAATAC GTGCAAGCAT TTACTGGAAA GCACTTGGGT CATATCATAT 1696

GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA 1756

TAAACATGTT AGTGTGAAAC TGTTCTAACA ATACAAATAG TATGGTATGC TTGTGCATTC 1816

TGCCTTCATC CCTTTCTATT TCTTTCTAAG TTATTTATTT AATAGGATGT TAAATATCTT 1876

TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTTCT TTTTATTCAG 1936

CACACCACAT GCATGTTCAC GACAAAGTGT TTTTAAAACT TGGCGAACAC TTCAAAAATA 1996

GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTTGCA 2056

CTTCTGCAGT AATAACCATC AACAATAAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG 2116

AGATGTCTGC TATCATTTGA AAACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA 2176

GACCAGAAGG CCAAATTCTT CTCTTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA 2236

AAAAGGAAAA TTAATTGCTA AATACATTTA AATAGCCTAG CCTCATTATT TACTCATGAT 2296

TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA 2356

TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT 2416

Figure 3C

```
CCCAGGGGCT TAAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA   2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAAACCAA ATAAAACTTG TTTTCTGTAA   2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCATT TTGTTAGAGC   2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT   2656
AAATACATAA GCCTTATTTG CAGTGTCTGT AGTGATTTTA AAAATGTAGA AAAATACTAT   2716
TTGTTCTAAA TACTTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT   2776
CATATTTCTT GTTTTGAAAA AGCATTTTAT TGTTTGGACA CAGTATTTTG GTACAAAAAA   2836
AAAGACTCAC TAAATGTGTC TTACTAAAGT TTAACCTTTG GAAATGCTGG CGTTCTGTGA   2896
TTCTCCAACA AACTTATTTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATTT   2956
TTAAAAATTG CTTTATTAAG AAATTTTTTG TATAATCCCA TAAAAGGTCA TATTTTTCCC   3016
ATTCTTCAAA AAAACTGTAT TTCAGAAGAA ACACATTTGA GGCACTGTCT TTTGGCTTAT   3076
AGTTTAAATT GCATTTCATC ATACTTTGCT TCCAACTTGC TTTTTGGCAA ATGAGATTAT   3136
AAAAATGTTT AATTTTTGTG GTTGGAATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC   3196
TGTGAGCTAT AATGTAATGC ATTCCTATCC AAACTAGGTA TCTTTTTTTC CTTTATGTTG   3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCCA CAACCTAAAT TAAATGTTTG   3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT   3376
TATTTCACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG   3436
TACTCAAGAC ACTAAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT   3496
AGAAAACATC TCCCCTGTCT CTCCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG   3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTTGGGAGA CTGTGGGAAG ATGGCTTGAG   3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA   3676
AAACAAAACA AATGTAGCCA TGCGTGGTGG CATATACCTG TGGTCCCAAC TACTCAGGAG   3736
GCTGAAACGG AAGGATCTCT TGGGCCCCAG GAGTTTGAGG CTGCAGTGAG CTATAATCTT   3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA   3856
AAAGAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA   3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA   3976
GATTGTTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA   4036
```

Figure 3D

ATGGAAATAG AATTCTGGTC CCTTTTGCAA CTACTGAAGA AAAAAAAAAG CAGTTTCAGC 4096

CCTGAATGTT GTAGATTTGA AAAAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA 4156

TTCGCCCTAT AGTGAGTCGT A 4177

Figure 4A

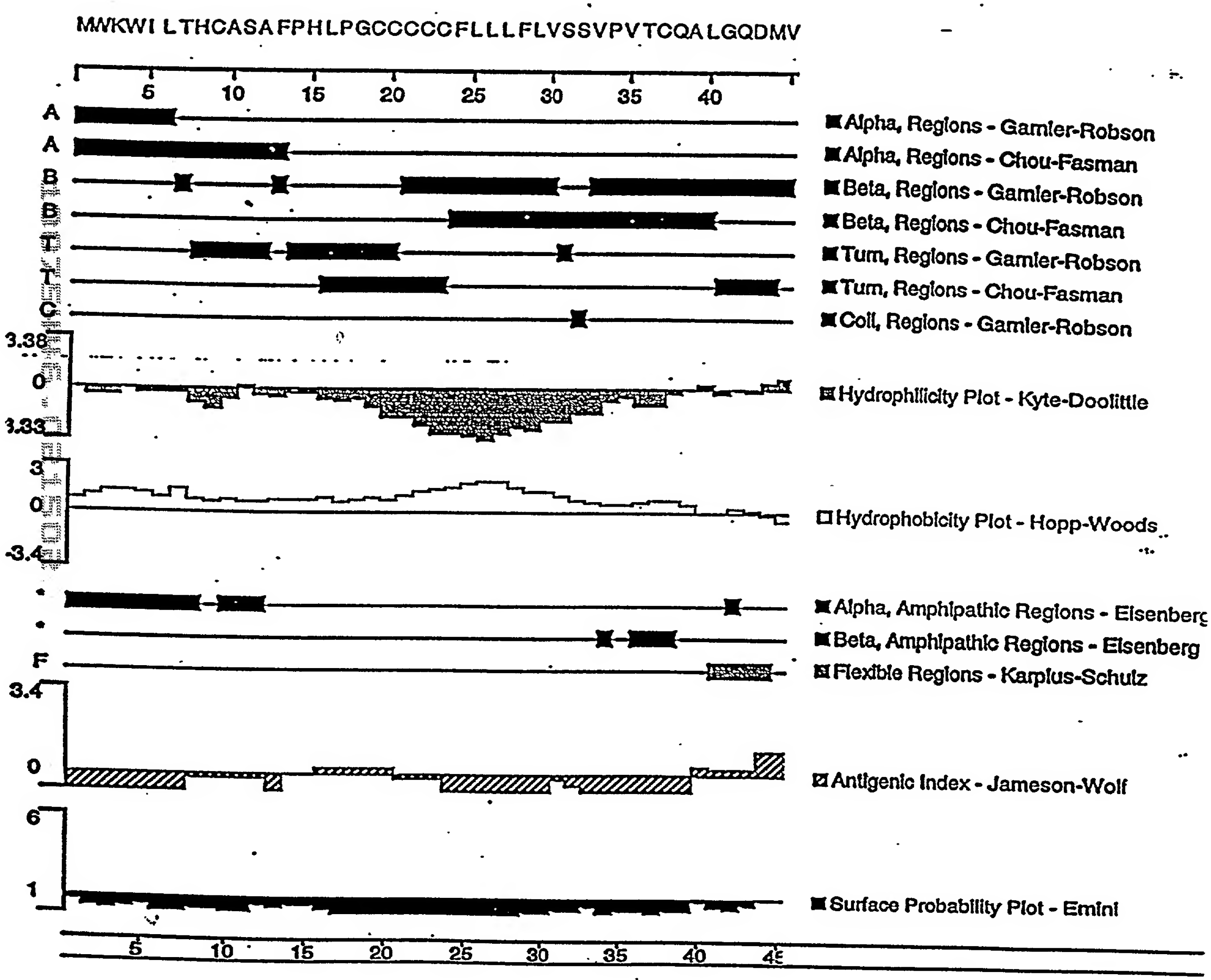
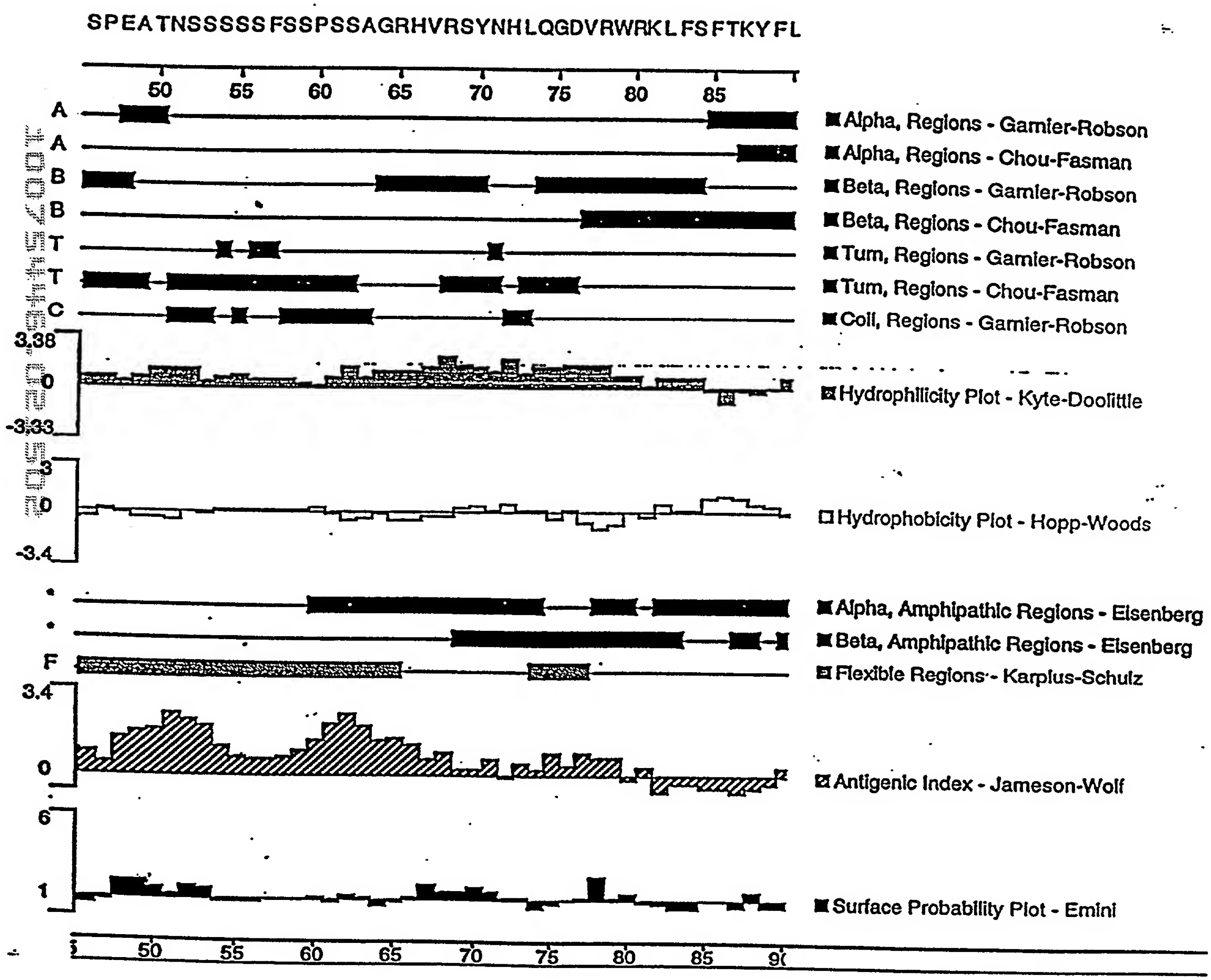
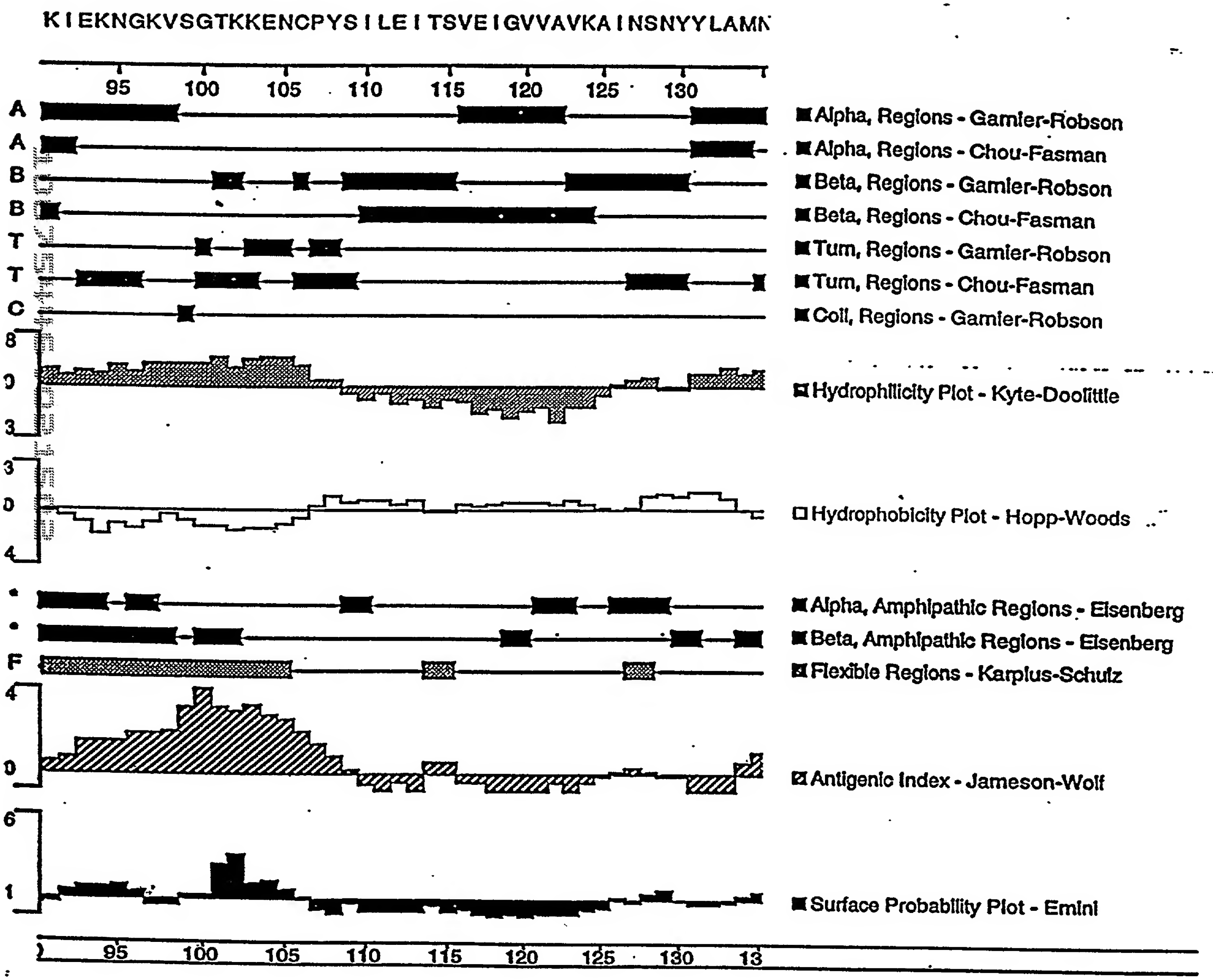

MWKWILTHCASAFPHLPGCCCCCFLLLFLVSSVPVTCQALGQDMV
5 10 15 20 25 30 35 40
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
3.38
0
3.33
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
5 10 15 20 25 30 35 40 45

Figure 4B



SPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFL
50
55
60
65
70
75
80
85
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
3.38
0
-3.33
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
50
55
60
65
70
75
80
85

Figure 4C



KIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMN
95 100 105 110 115 120 125 130
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
F
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

Figure 4D

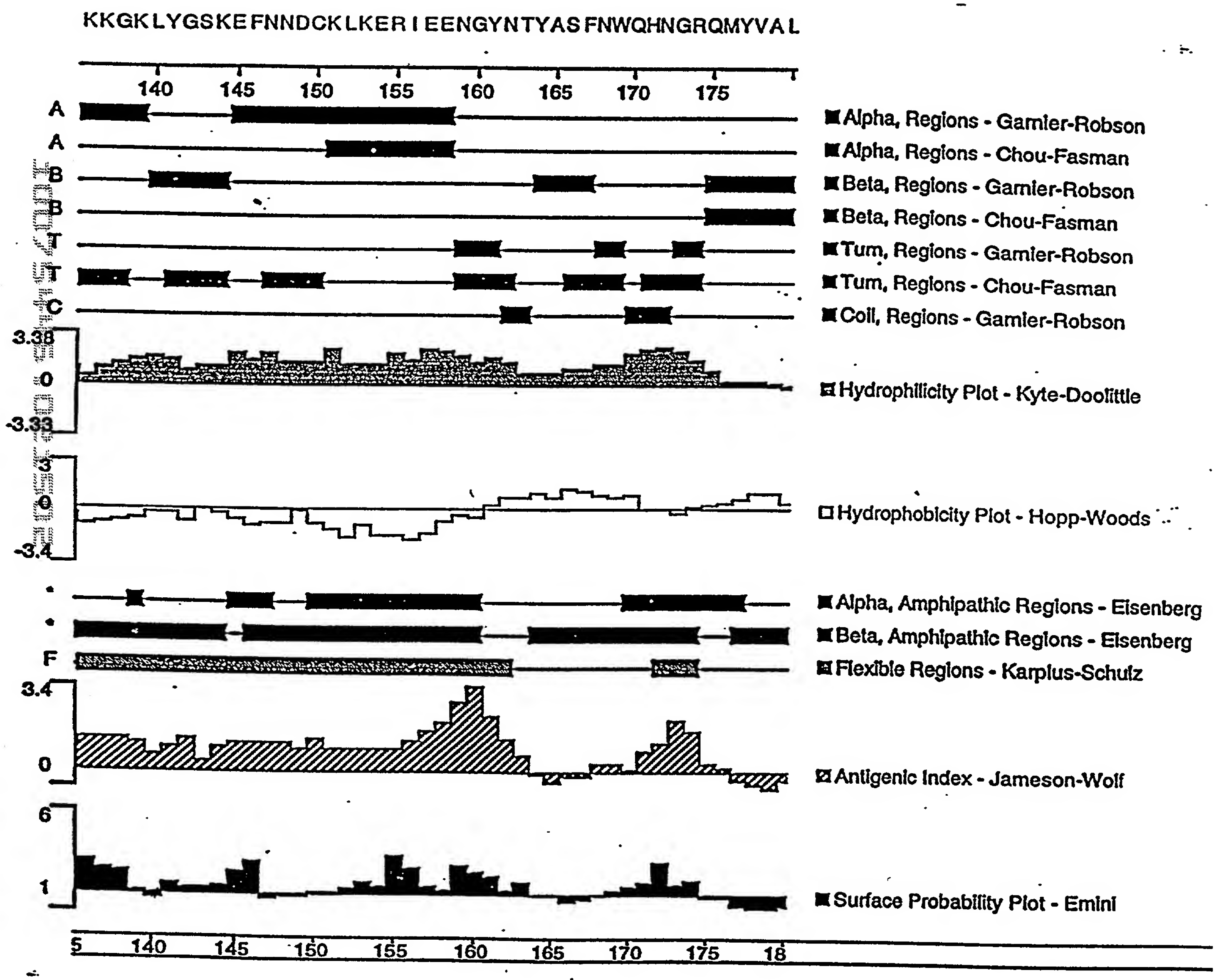
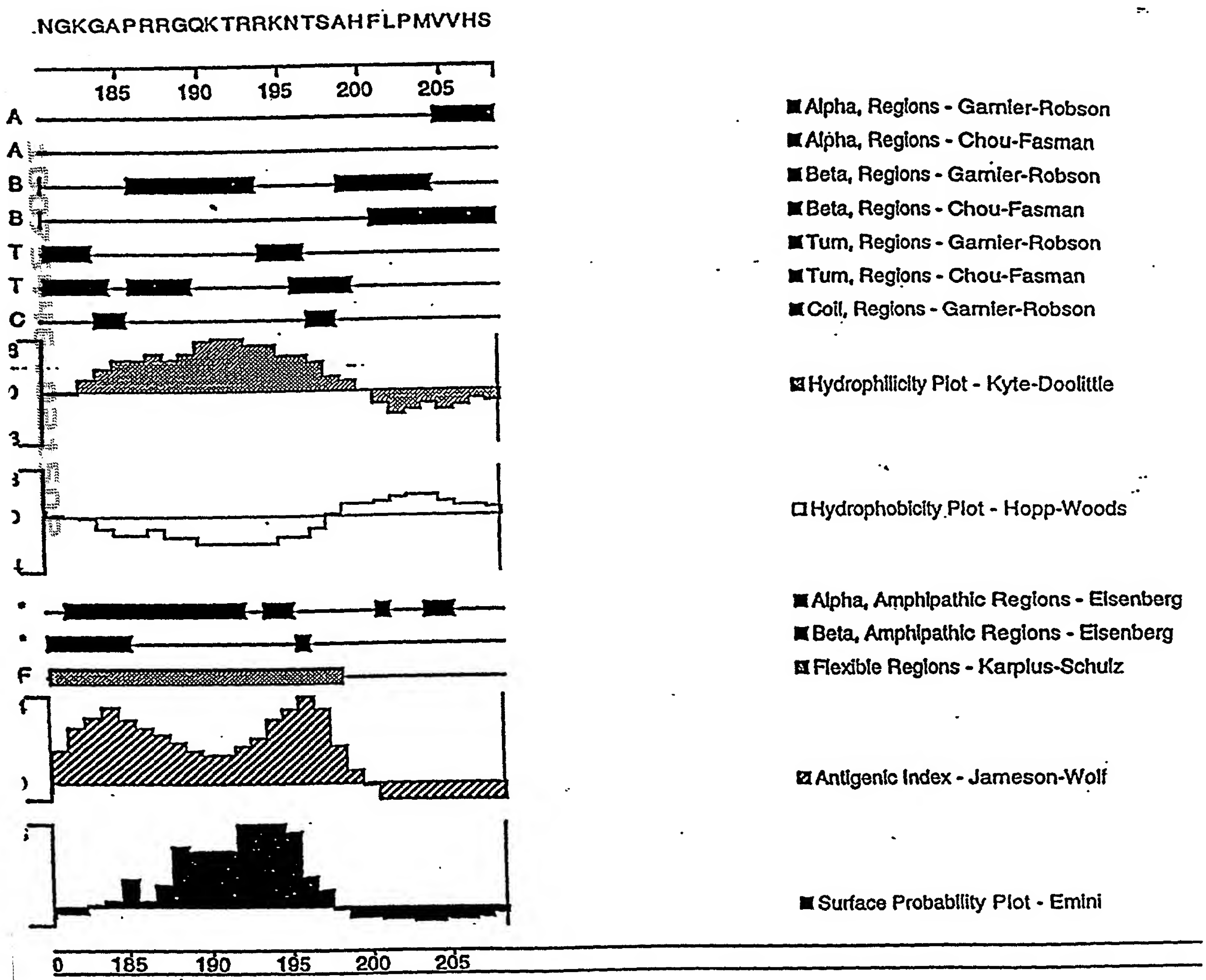

KKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVAL
140
145
150
155
160
165
170
175
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini

Figure 4E



.NGKGAPRRGQKTRRKNTSAHFLPMVVHS
185
190
195
200
205
A
A
B
B
T
T
C
F
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
Hydrophobicity Plot - Hopp-Woods
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
Antigenic Index - Jameson-Wolf
Surface Probability Plot - Emini
0
185
190
195
200
205

Figure 5

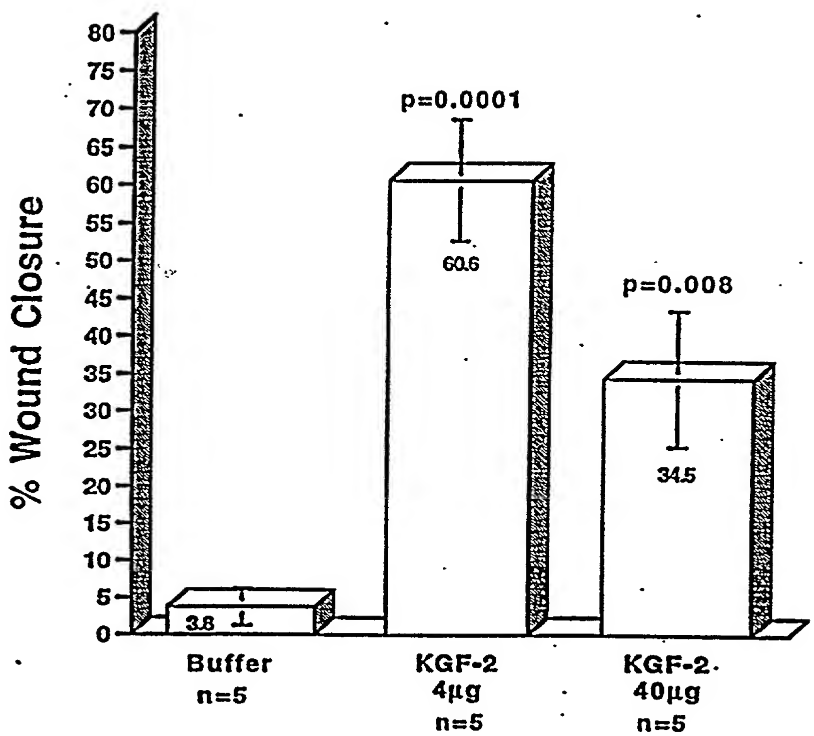
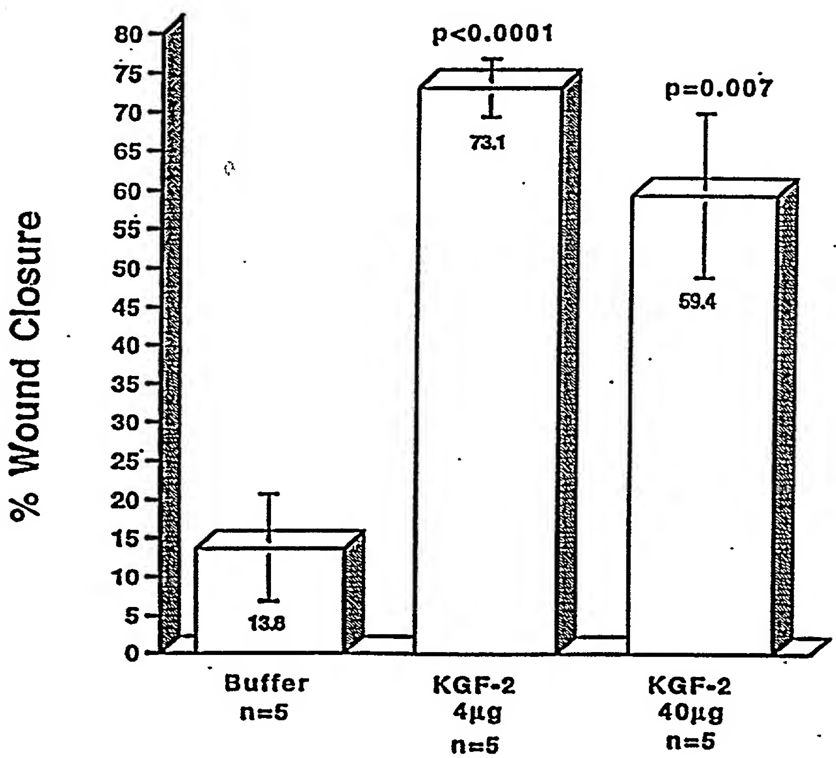
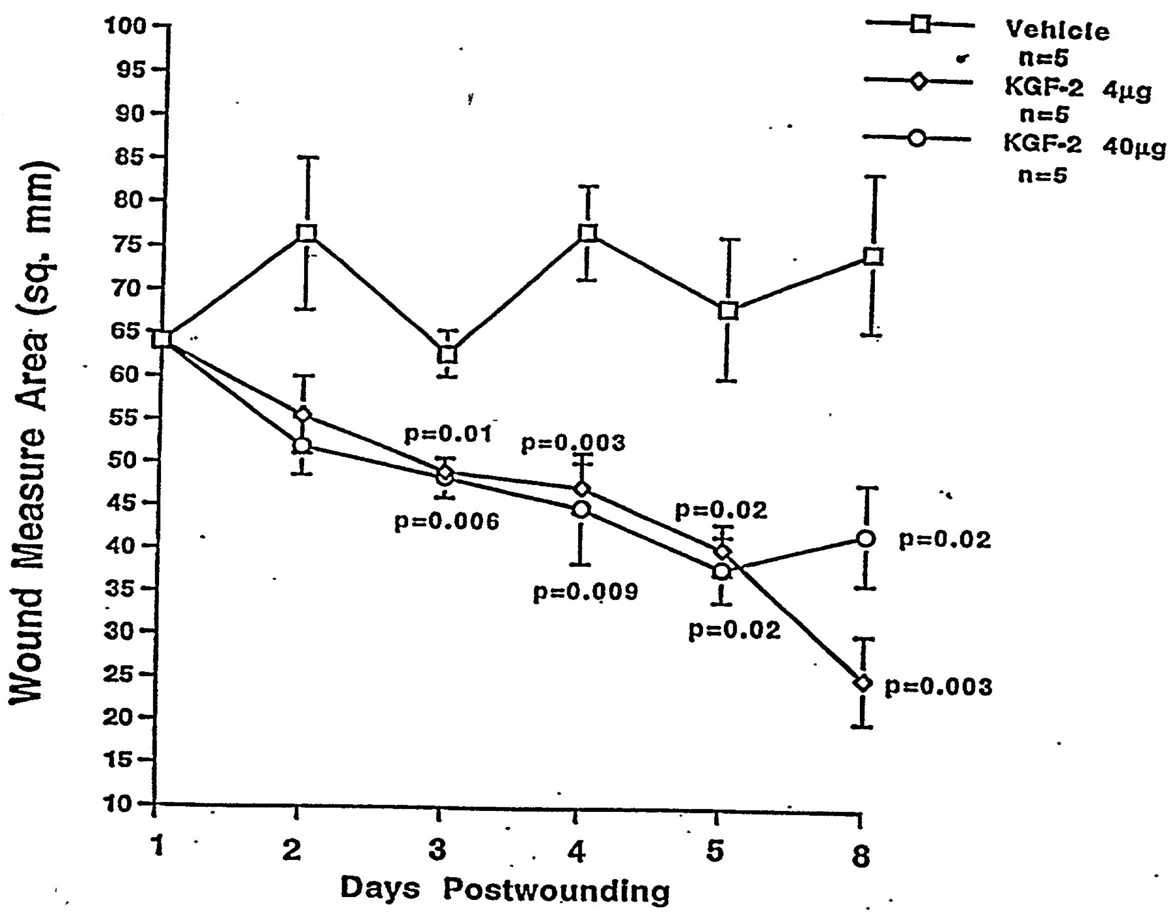

% Wound Closure
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
p=0.0001
60.6
p=0.008
34.5
3.8
Buffer
n=5
KGF-2
4µg
n=5
KGF-2
40µg
n=5

Figure 6



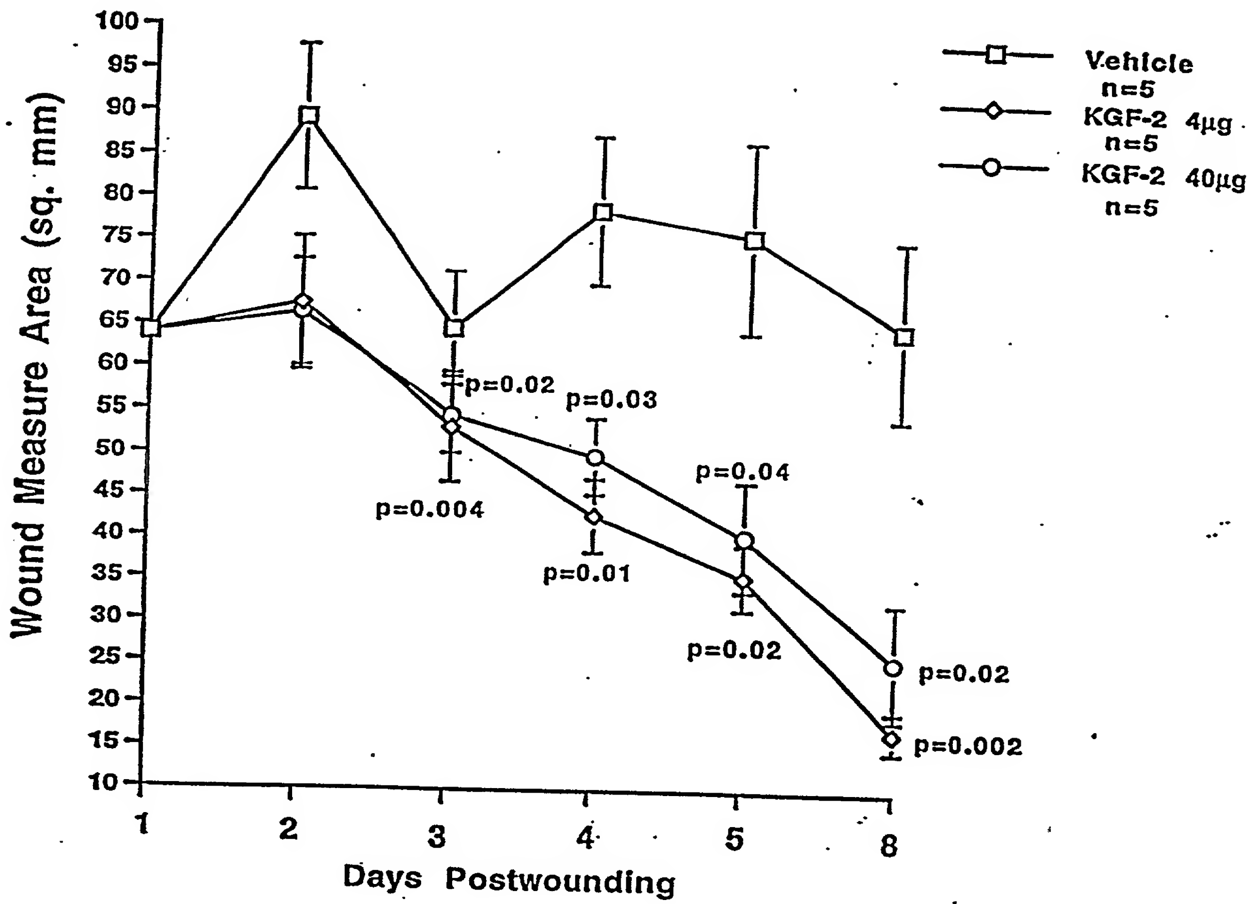
% Wound Closure
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
p<0.0001
p=0.007
13.8
73.1
59.4
Buffer n=5
KGF-2 4µg n=5
KGF-2 40µg n=5

Figure 7



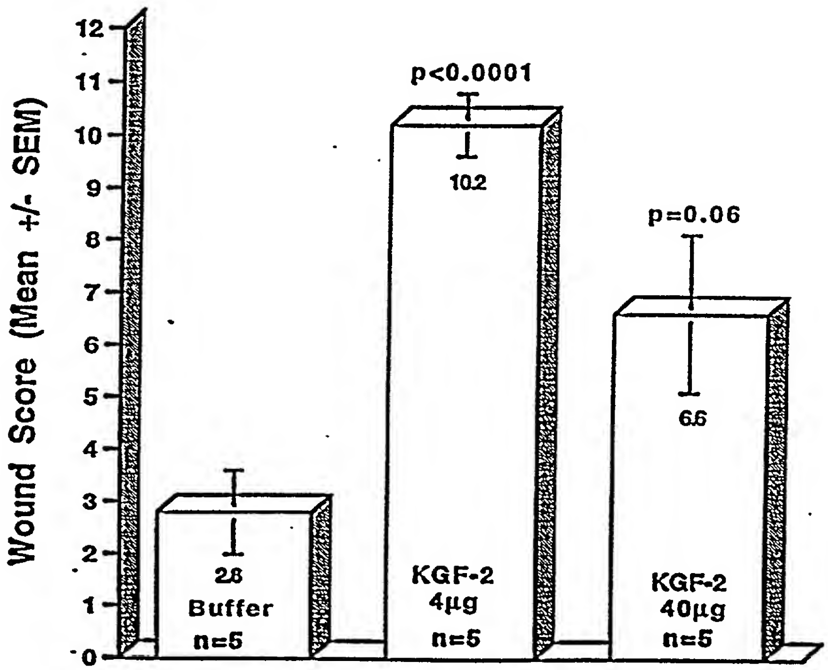
Vehicle n=5
KGF-2 4µg n=5
KGF-2 40µg n=5
Wound Measure Area (sq. mm)
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
p=0.01
p=0.003
p=0.006
p=0.02
p=0.02
p=0.009
p=0.02
p=0.003
1
2
3
4
5
8
Days Postwounding

Figure 8



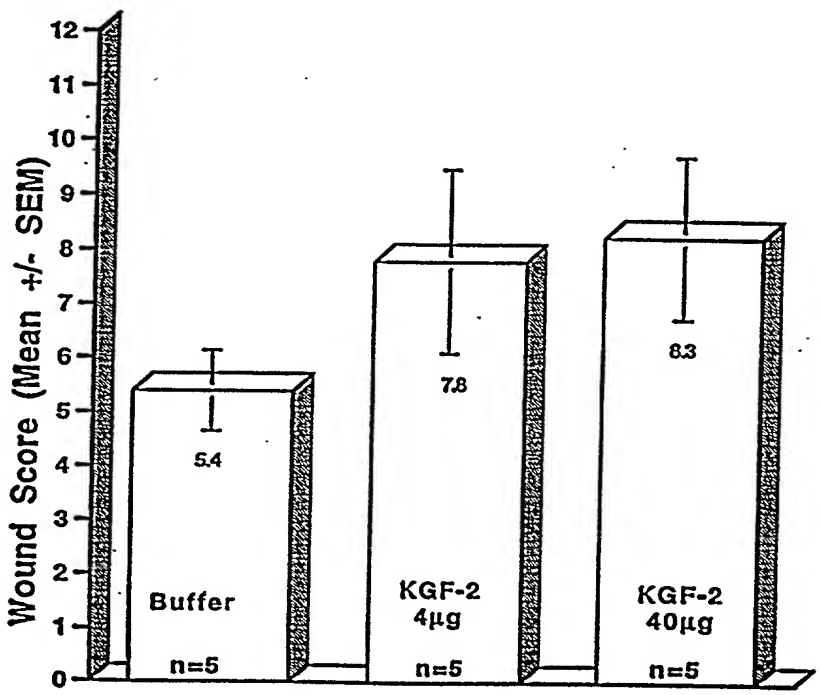
Wound Measure Area (sq. mm)
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
1
2
3
4
5
8
Days Postwounding
Vehicle
n=5
KGF-2 4µg
n=5
KGF-2 40µg
n=5
p=0.02
p=0.03
p=0.004
p=0.04
p=0.01
p=0.02
p=0.02
p=0.002

Figure 9



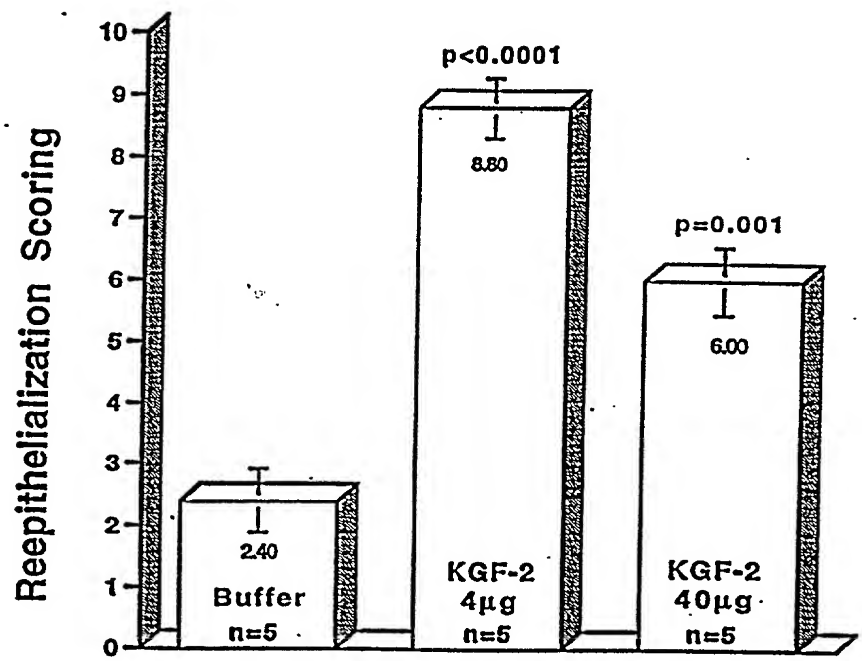
1-3 Minimal cell accumulation, no granulation
4-6 Immature granulation, inflammatory cells, capillaries
10-12 Fibroblasts, collagen, epithelium

Figure 10



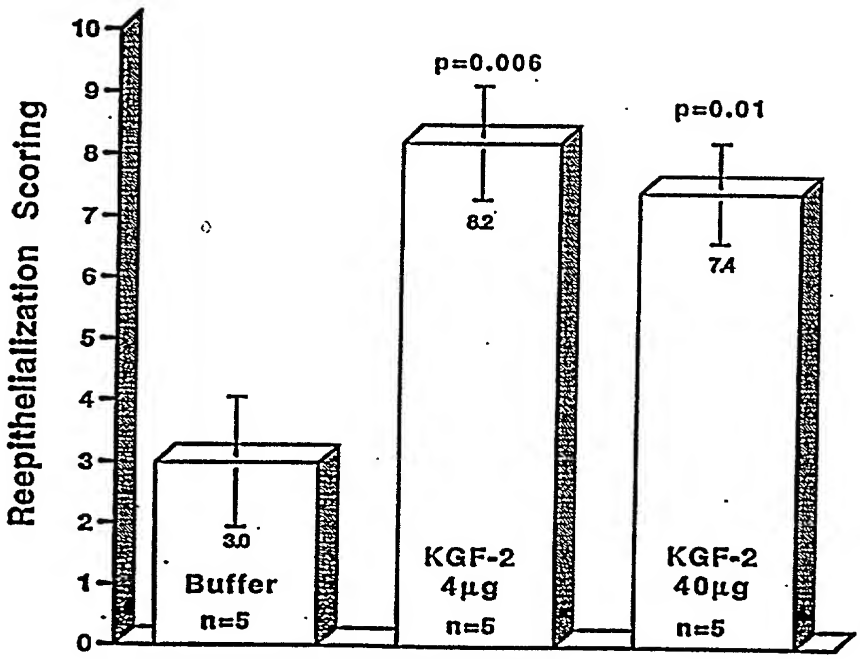
1-3 Minimal cell accumulation, no granulation
4-6 Immature granulation, inflammatory cells, capillaries
7-9 Granulation tissue, cells, fibroblasts, new epithelium
10-12 Fibroblasts, collagen, epithelium

Figure 11



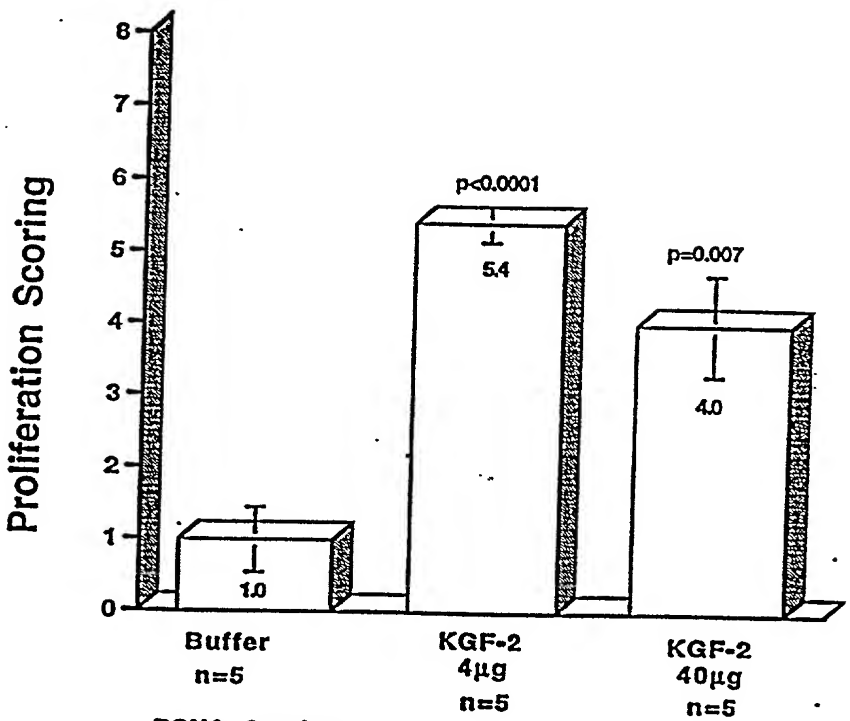
Anti-cytokeratin Immunostaining
0 - No closure
5 - Slight to moderate closure
10 - Complete closure

Figure 12



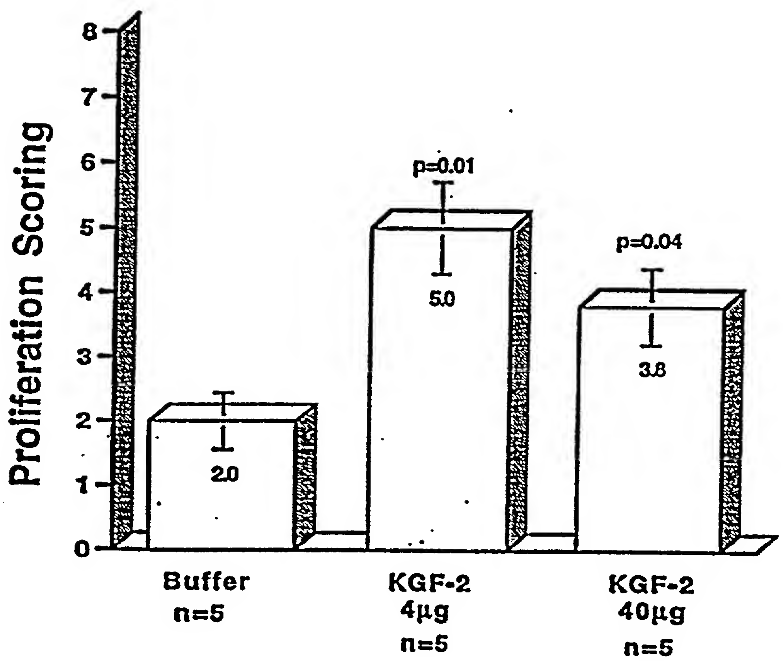
Anti-cytokeratin Immunostaining
0 - No closure
5 - Slight to moderate closure
10 - Complete closure

Figure 13



PCNA Scoring
0-2 Slight proliferation
3-5 Moderate proliferation
6-8 Intense proliferation

Figure 14



PCNA Scoring
0-2 Slight proliferation
3-5 Moderate proliferation
6-8 Intense proliferation

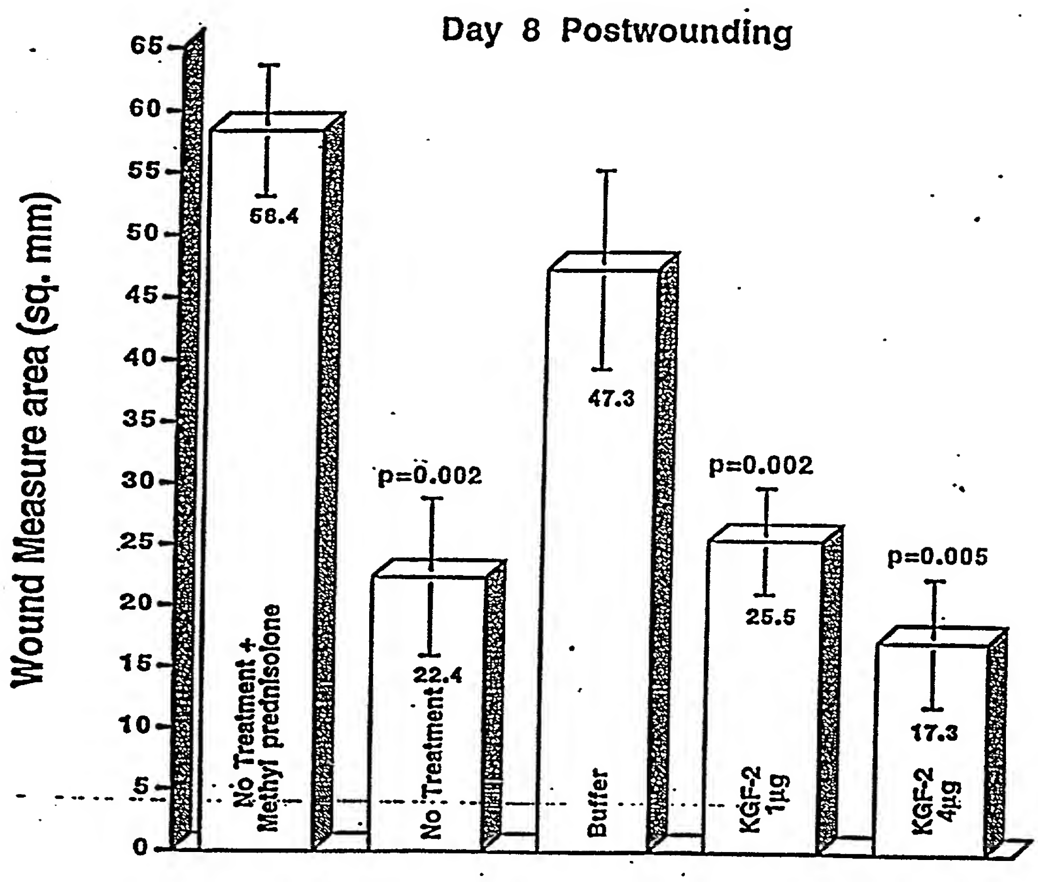
Figure 15

ATGAGAGGATCGCATCACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC
AGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCC
CGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTC
GTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTG
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG
CAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAG
AATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT
ACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTAT
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG
GAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MRGSHHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD
VRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSN
YYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS

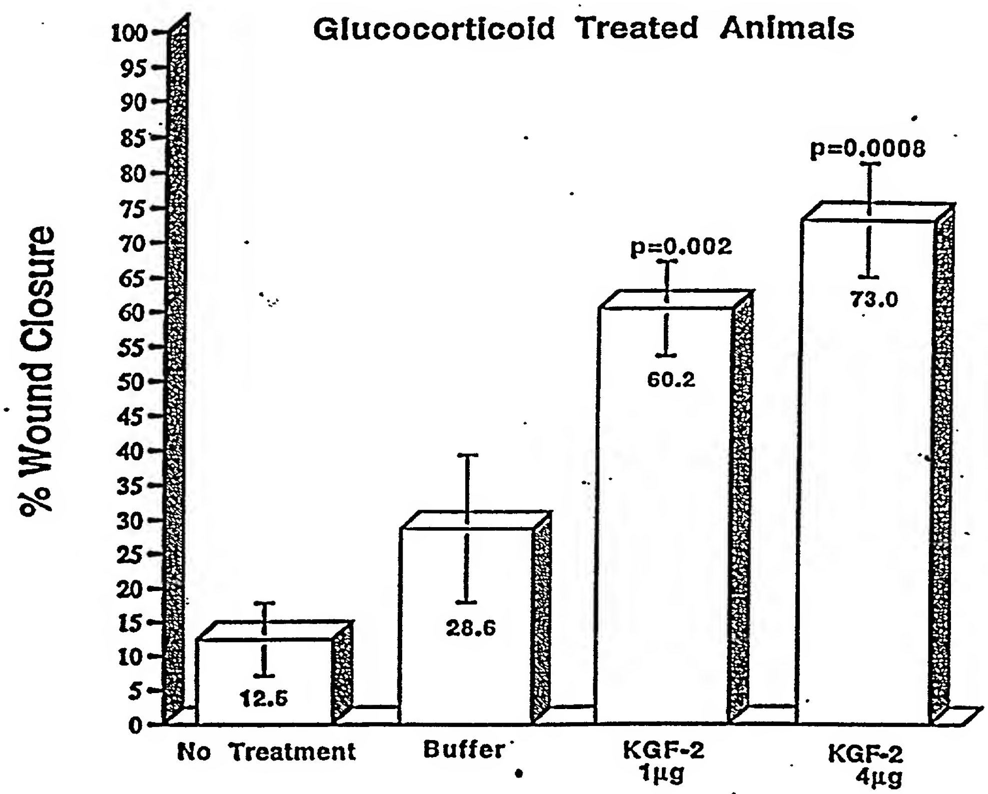
kgf-2 synthetic cys37 Bam HI
AAAGGATCCTGCCAGGCTCTGGGTCAGGACATG

Figure 16



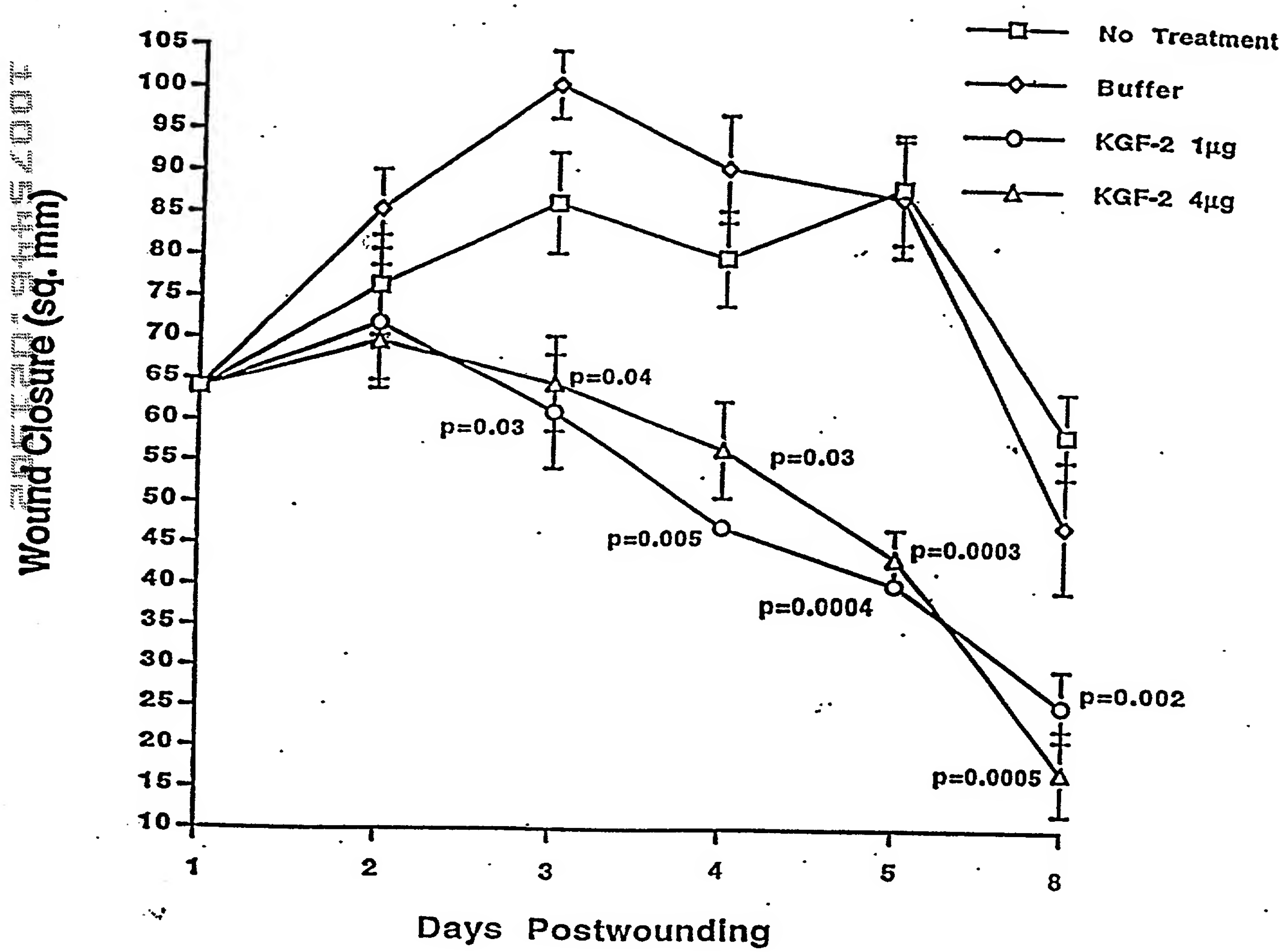
Day 8 Postwounding
Wound Measure area (sq. mm)
65
60
55
50
45
40
35
30
25
20
15
10
5
0
58.4
No Treatment + Methyl prednisolone
p=0.002
22.4
No Treatment
47.3
Buffer
p=0.002
25.5
KGF-2 1µg
p=0.005
17.3
KGF-2 4µg

Figure 17



Glucocorticoid Treated Animals
% Wound Closure
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
p=0.002
p=0.0008
12.5
28.6
60.2
73.0
No Treatment
Buffer
KGF-2 1μg
KGF-2 4μg

Figure 18



No Treatment
Buffer
KGF-2 1µg
KGF-2 4µg
Wound Closure (sq. mm)
105
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
p=0.04
p=0.03
p=0.03
p=0.005
p=0.0003
p=0.0004
p=0.002
p=0.0005
1
2
3
4
5
8
Days Postwounding

Figure 19A

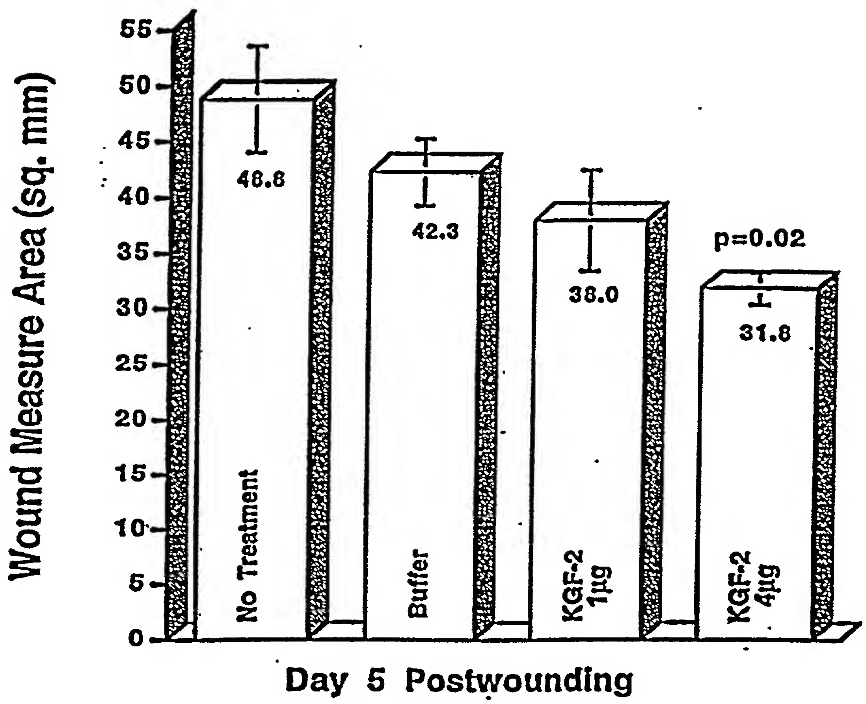
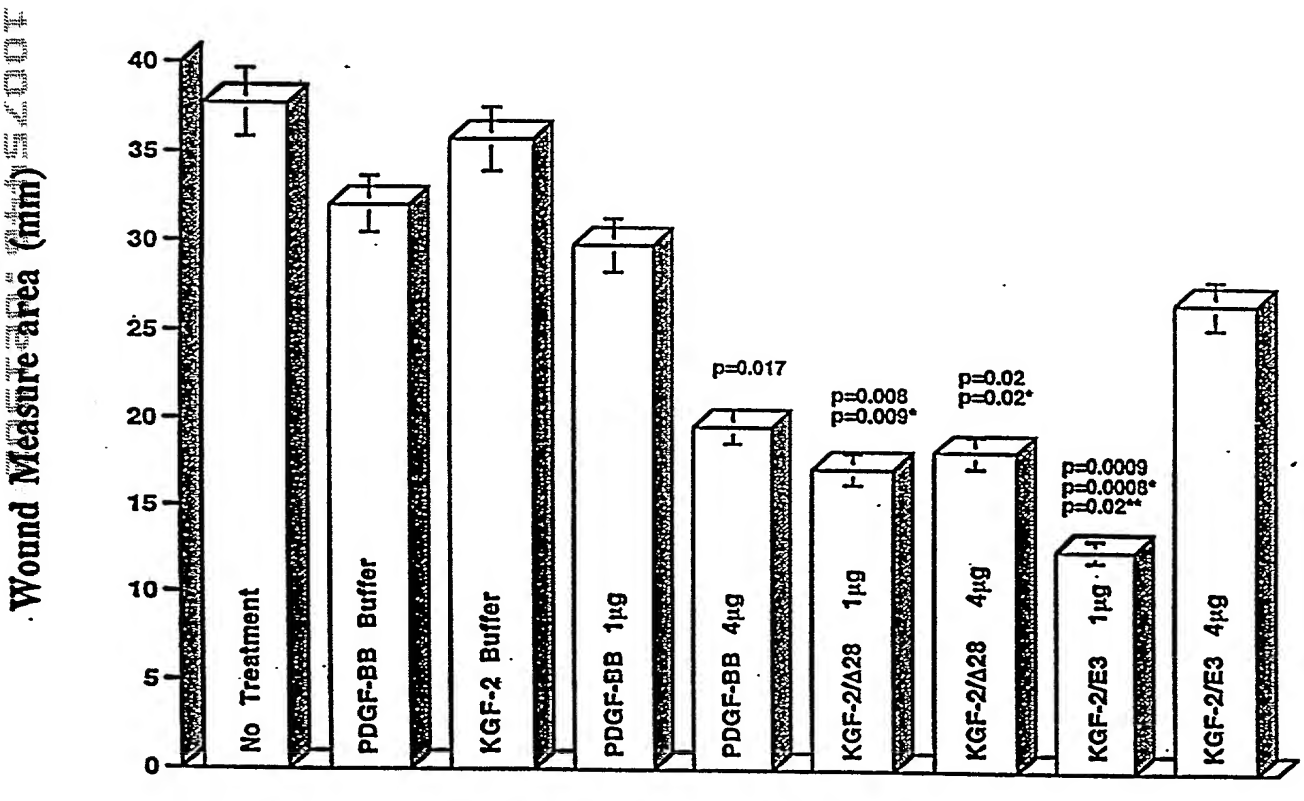
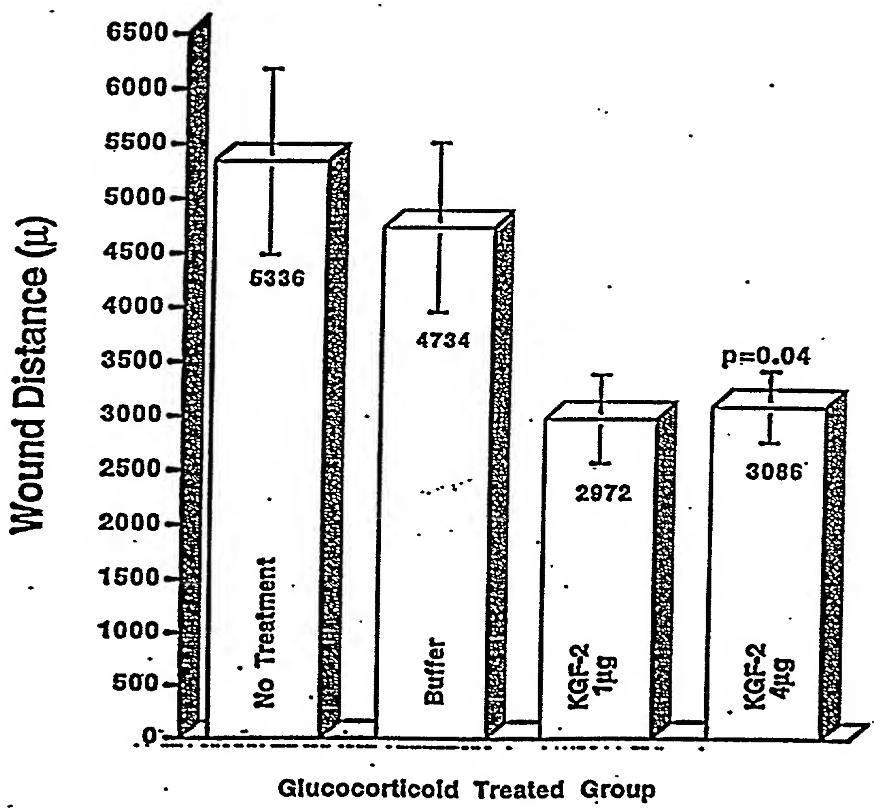

Wound Measure Area (sq. mm)
55
50
45
40
35
30
25
20
15
10
5
0
48.8
42.3
38.0
p=0.02
31.8
No Treatment
Buffer
KGF-2 1µg
KGF-2 4µg
Day 5 Postwounding

Figure 19B



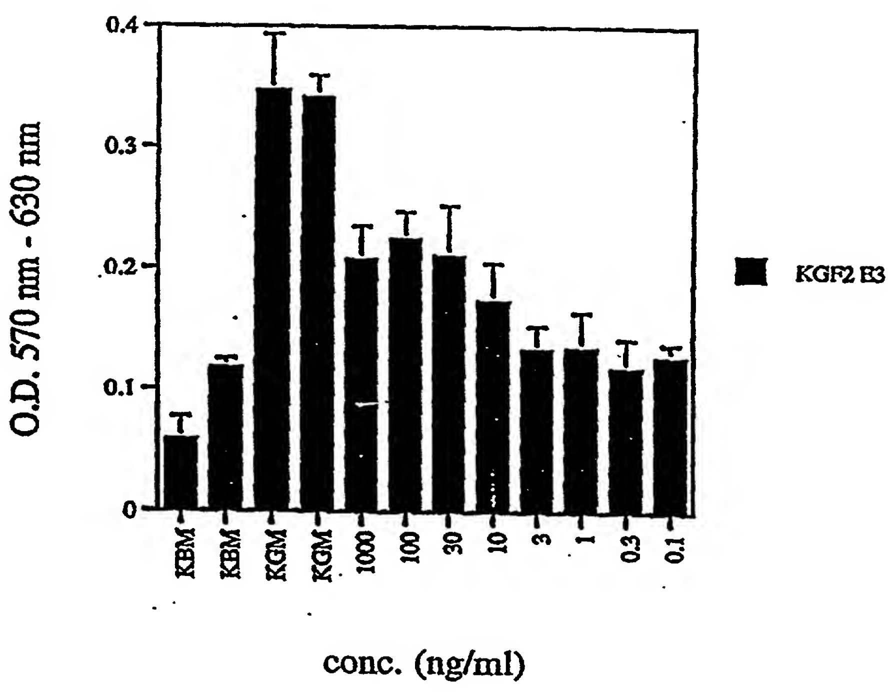
Day 10 Postwounding

Figure 20



Wound Distance (μ)
6500
6000
5500
5000
4500
4000
3500
3000
2500
2000
1500
1000
500
0
5336
4734
2972
3086
p=0.04
No Treatment
Buffer
KGF-2 1μg
KGF-2 4μg
Glucocorticoid Treated Group

Figure 21A



0.4
0.3
0.2
0.1
0
O.D. 570 nm - 630 nm
KBM
KBM
KGM
KGM
1000
100
30
10
3
1
0.3
0.1
conc. (ng/ml)
KGF2 B3

Figure 21B

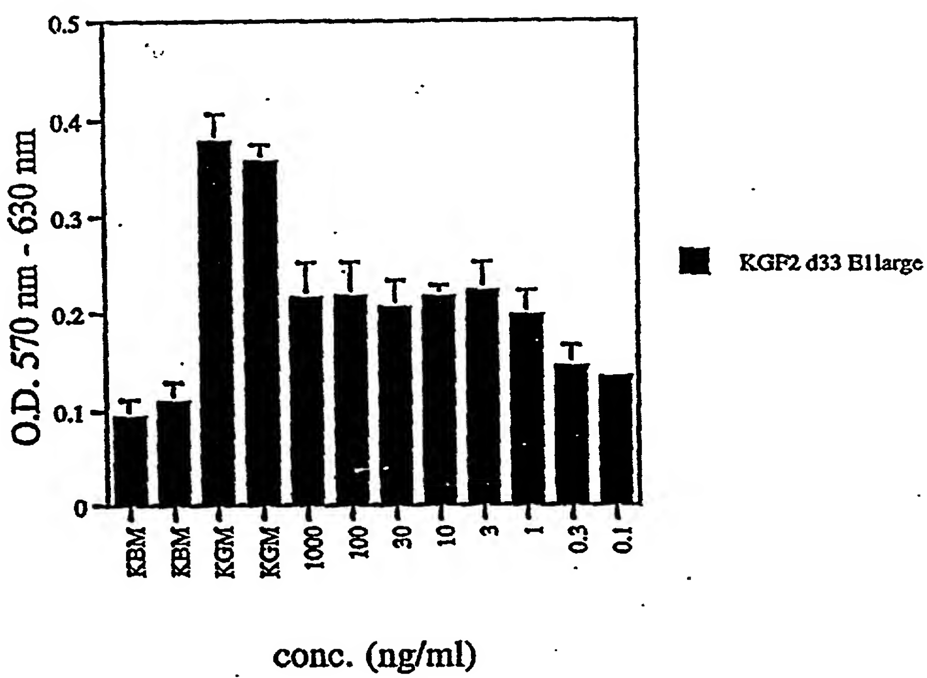
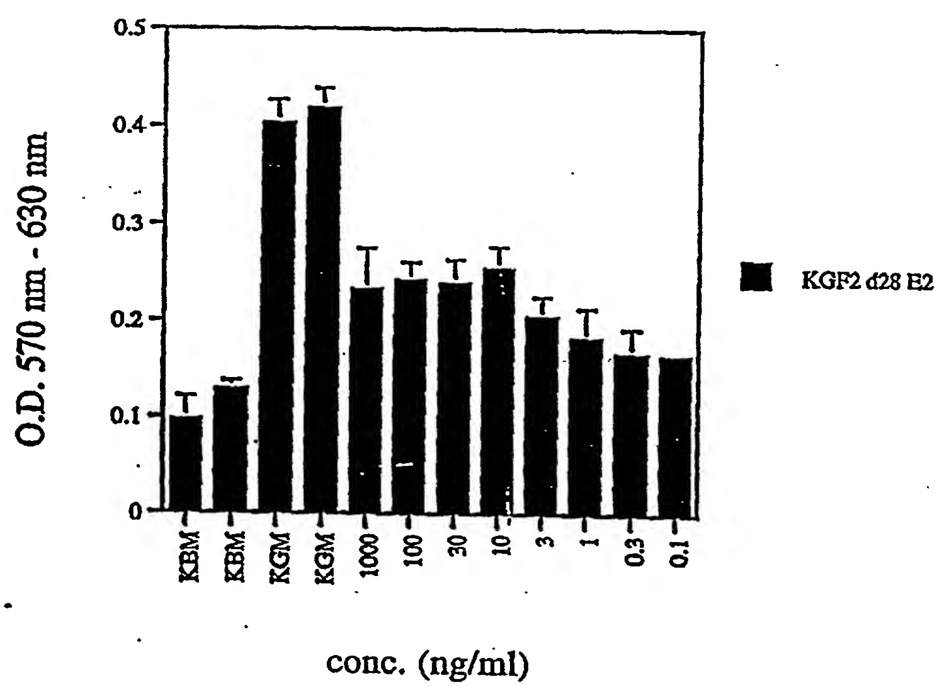

0.5
0.4
0.3
0.2
0.1
0
O.D. 570 nm - 630 nm
KBM
KBM
KGM
KGM
1000
100
30
10
3
1
0.3
0.1
conc. (ng/ml)
KGF2 d33 B1large

Figure 21C



O.D. 570 nm - 630 nm
0.5
0.4
0.3
0.2
0.1
0
KBM
KBM
KGM
KGM
1000
100
30
10
3
1
0.3
0.1
conc. (ng/ml)
KGF2 d28 E2

Figure 22A

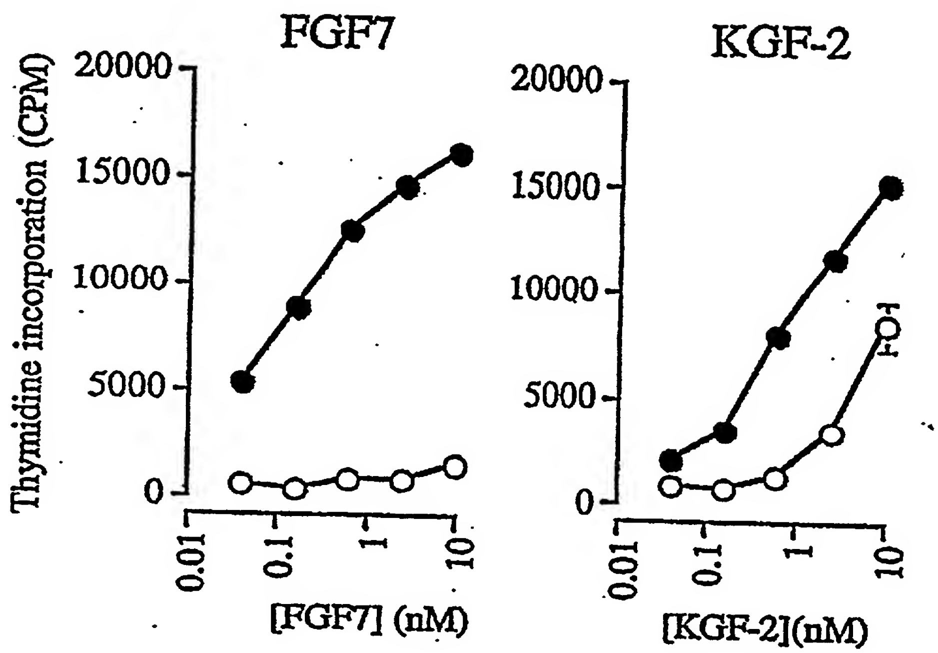
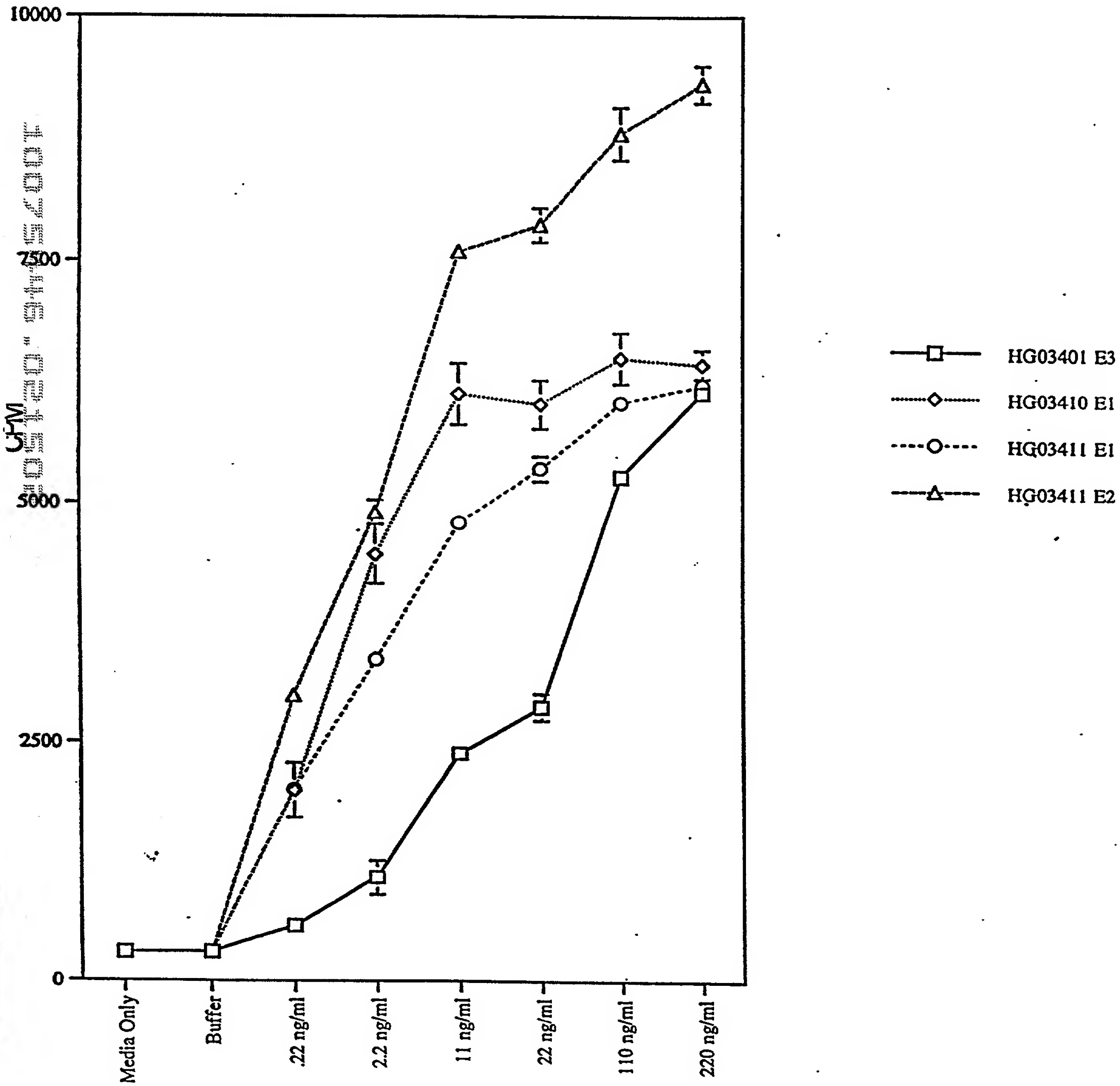
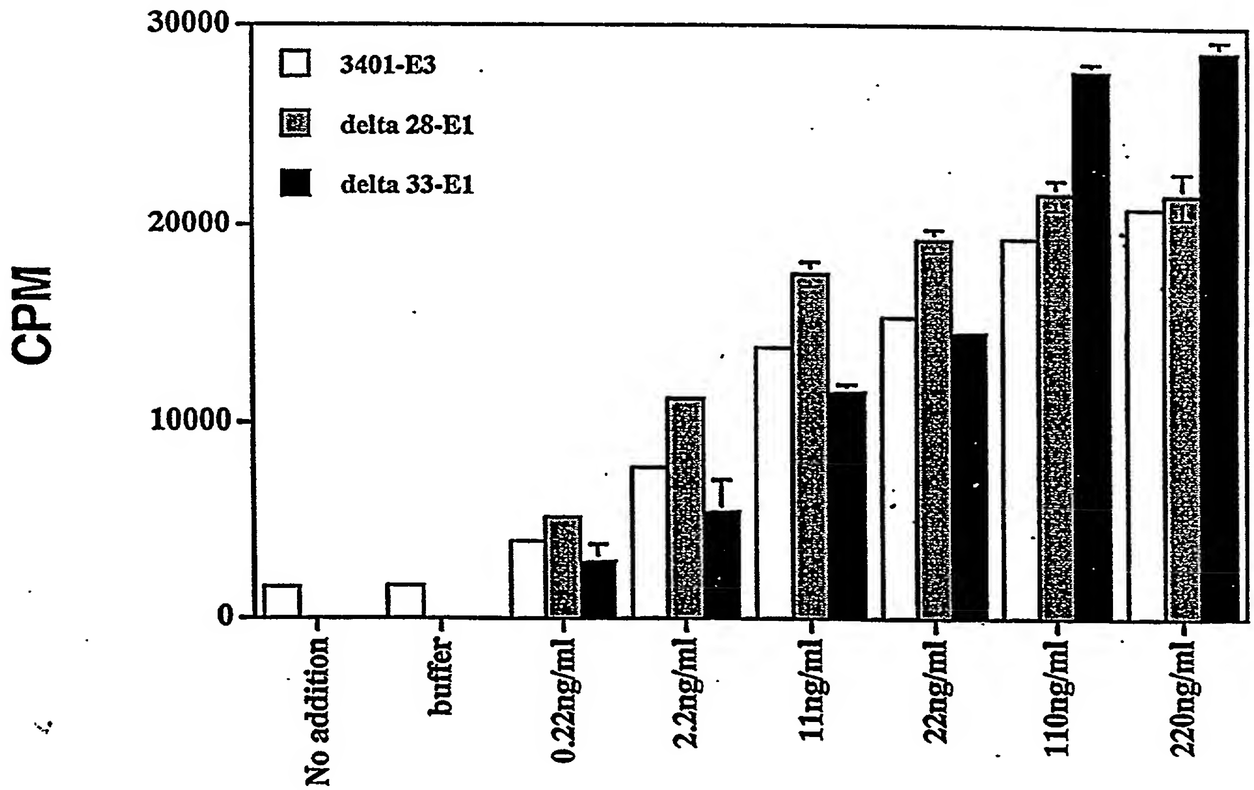

FGF7
KGF-2
Thymidine incorporation (CPM)
20000
15000
10000
5000
0
0.01
0.1
1
10
[FGF7] (nM)
[KGF-2](nM)

Figure 22B



10000
7500
5000
2500
0
CPM
Media Only
Buffer
.22 ng/ml
2.2 ng/ml
11 ng/ml
22 ng/ml
110 ng/ml
220 ng/ml
HG03401 E3
HG03410 E1
HG03411 E1
HG03411 E2

Figure 22C



CPM
30000
20000
10000
0
3401-E3
delta 28-E1
delta 33-E1
No addition
buffer
0.22ng/ml
2.2ng/ml
11ng/ml
22ng/ml
110ng/ml
220ng/ml

Figure 23

ATGTGGAAATGGATACTGACCCACTGCGCTTCTGCTTTCCCGCACCTGCCGGGTTGCTGC 60
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys

TGCTGCTGCTTCCTGCTGCTGTTCCTGGTTTCTTCTGTTCCGGTTACCTGCCAGGCTCTG 120
Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu

GGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTTCTCTTCCCCG 180
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Ser Ser Phe Ser Ser Pro

ACTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT 240
Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg

AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCTGGG 300
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly

ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val

GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTC 420
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu

TATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480
Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly

TACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu

AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC 600
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His

TTTCTTCCAATGGTGGTACACTCATAG 627
Phe Leu Pro Met Val Val His Ser •

Figure 24A

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCCTCT 60
Met Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser

TCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAG 120
Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln

GGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA 180
Gly Asp Val Arg Trp Arg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys

AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACA 240
Asn Gly Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr

TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATG 300
Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met

AACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAG 360
Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu

AGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG 420
Arg Ile Glu Glu Asn Gly Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg

CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480
Gln Met Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg

AAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG 525
Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser •

Figure 24B

```
ATGACTTGCCAGGCACTGGGTCAAGACATGGTTTCCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA
+---------+---------+---------+---------+---------+---------+---------+ 70
TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGGCCTTCGATGGTTGTCGAGGTCGAGATCGAAGT

 M  T  C  Q  A  L  G  Q  D  M  V  S  P  E  A  T  N  S  S  S  S  S  F

GCAGCCCATCTAGCGCAGGTCGTCACGTTCGCTCTTACAACCACTTACAGGGTGATGTTCGTTGGCGCAA
+---------+---------+---------+---------+---------+---------+---------+ 140
CGTCGGGTAGATCGCGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACTACAAGCAACCGCGTT

 S  S  P  S  S  A  G  R  H  V  R  S  Y  N  H  L  Q  G  D  V  R  W  R  K

ACTGTTCAGCTTTACCAAGTACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAG
+---------+---------+---------+---------+---------+---------+---------+ 210
TGACAAGTCGAAATGGTTCATGAAGGACTTTTAGCTTTTTTTGCCATTTCAAAGACCCTGGTTCTTCCTC

 L  F  S  F  T  K  Y  F  L  K  I  E  K  N  G  K  V  S  G  T  K  K  E

AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACA
+---------+---------+---------+---------+---------+---------+---------+ 280
TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTTAGCCTCAACAACGGCAGTTTCGGTAATTGT

 N  C  P  Y  S  I  L  E  I  T  S  V  E  I  G  V  V  A  V  K  A  I  N

GCAACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAA
+---------+---------+---------+---------+---------+---------+---------+ 350
CGTTGATAATGAATCGGTACTTGTTCTTCCCCTTTGAGATACCGAGTTTTCTTAAATTGTTACTGACATT

 S  N  Y  Y  L  A  M  N  K  K  G  K  L  Y  G  S  K  E  F  N  N  D  C  K

GCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG
+---------+---------+---------+---------+---------+---------+---------+ 420
CGACTTCCTCTCCTATCTCCTTTTACCTATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCTCC

 L  K  E  R  I  E  E  N  G  Y  N  T  Y  A  S  F  N  W  Q  H  N  G  R

CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCT
+---------+---------+---------+---------+---------+---------+---------+ 490
GTTTACATACACCGTAACTTACCTTTTCCTCGAGGTTCCTCTCCTGTCTTTTGTGCTTCCTTTTTGTGGA

 Q  M  Y  V  A  L  N  G  K  G  A  P  R  R  G  Q  K  T  R  R  K  N  T

CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG
+---------+---------+---------+----> 525
GACGAGTGAAAGAAGGTTACCACCATGTGAGTATC

 S  A  H  F  L  P  M  V  V  H  S  .
```

Figure 25

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCAT
TTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCT
CCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAAT
GGTGGTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 26

ATGGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAAT
CGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAA
GGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGA
TAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGG
CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACAC
GAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 27

ATGGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAA
AACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGAT
AACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTT
AGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTA
AGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGG
CAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAG
AGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTAC
ACTCATAG

MVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAM
NKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQ
KTRRKNTSAHFLPMVVHS.

Figure 28

ATGGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCAT
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCA
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAAC
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATC
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCA
ATGGTGGTACACTCATAG

MEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDC
KLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH
S.

Figure 29

ATGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC
TCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA
AATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTA
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAA
AACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGY
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 30

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACT
CTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAA
ATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGAGGCAAATGTATG
TGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAA
CACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MVKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMY
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

Figure 31

ATGGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAGGAGAG
GATAGAGGAAAATGGATACAATACCTATGCATCATTTAACTGGCAGCATAATGGGA
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAAC
ACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAATGGTGGTACACTCATAG

MGKLYGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT
RRKNTSAHFLPMVVHS.

Figure 32

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSNYYLAMNKKGKLYGSKEFNNDCKL
K

Figure 33

ATGGCTGGTCGTCACGTTCGTTCTTACAACCACCTGCAGGGTGACGTTCGTTGGCGT
AAACTGTTCTCTTTCACCAAATACTTCCTGAAAATCGAAAAAAACGGTAAAGTTTCT
GGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAAT
CGGAGTTGTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAA
GGGGAAACTCTATGGCTCAAAAGAATTTAACAATGACTGTAAGCTGAAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV
VAVKAINSNYYLAMNKKGKLYGSKEFNNDCKLK

Figure 34

C-37 To Ser

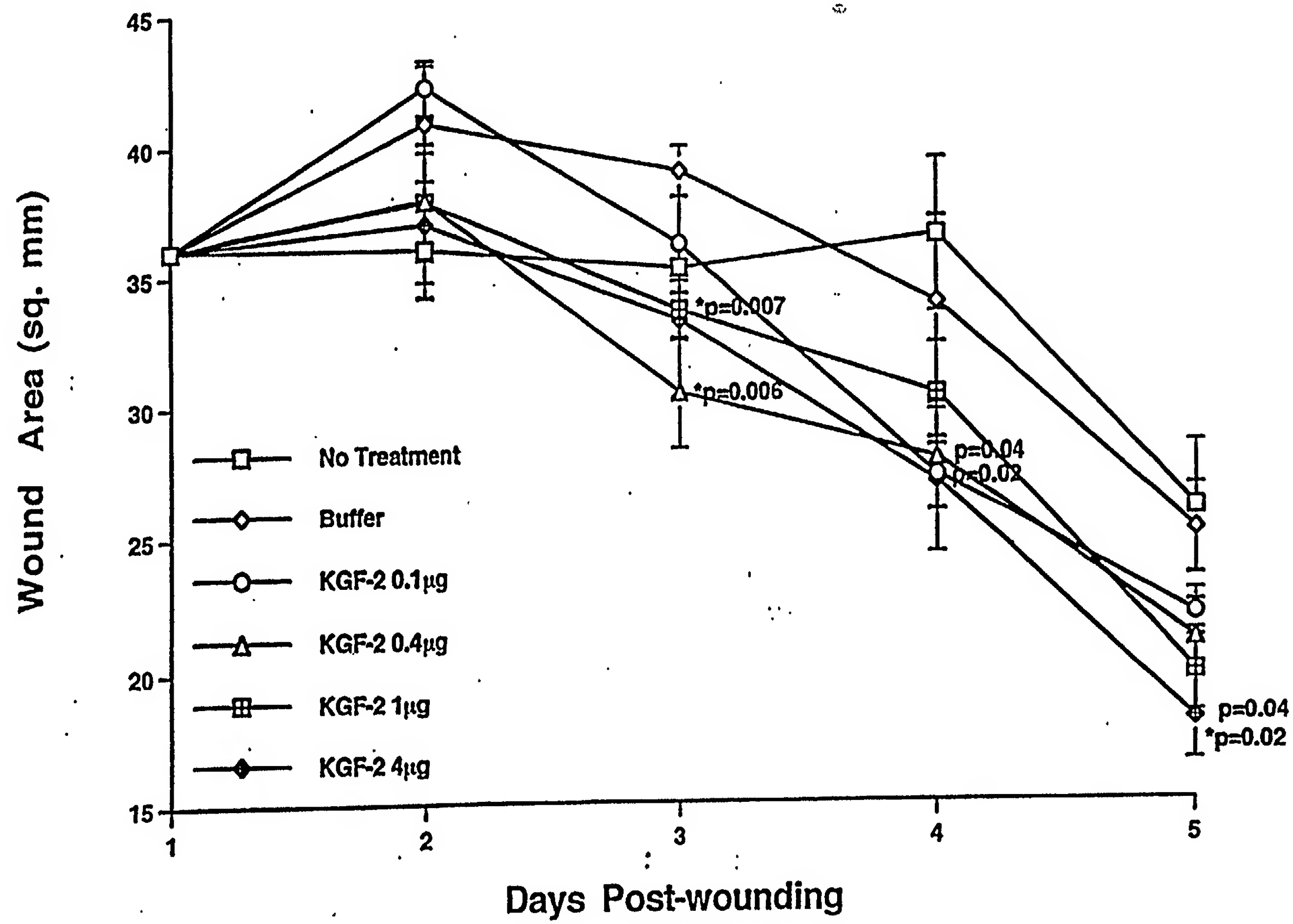
ATGACCTCTCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCAT
TTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCT
CCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAAT
GGTGGTACACTCATAG

Figure 35

: C-106 To Ser

ATGACCTGCCAGGCTCTGGGTCAGGACATGGTTTCTCCGGAAGCTACCAACTCTTCC
TCTTCCTCTTTCTCTTCCCCGTCTTCCGCTGGTCGTCACGTTCGTTCTTACAACCACCT
GCAGGGTGACGTTCGTTGGCGTAAACTGTTCTCTTTCACCAAATACTTCCTGAAAAT
CGAAAAAAACGGTAAAGTTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATCC
TGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAGCAAC
TATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTCAAAAGAATTTAACAA
TGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATACAATACCTATGCATCAT
TTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCT
CCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTTCTTCCAAT
GGTGGTACACTCATAG

Figure 36



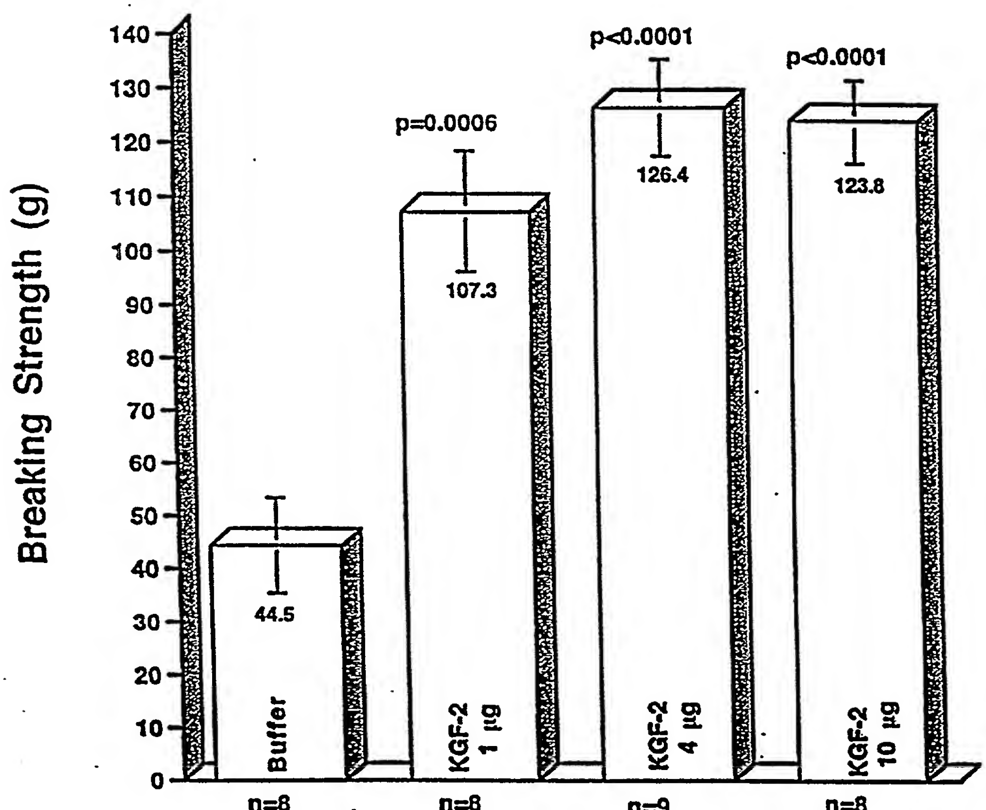
Wound Area (sq. mm)
45
40
35
30
25
20
15
1
2
3
4
5
Days Post-wounding
No Treatment
Buffer
KGF-2 0.1μg
KGF-2 0.4μg
KGF-2 1μg
KGF-2 4μg
*p=0.007
*p=0.006
p=0.04
p=0.02
p=0.04
*p=0.02

Figure 37

Effect of KGF-2 Δ33 on Normal Wound Healing Rat Model

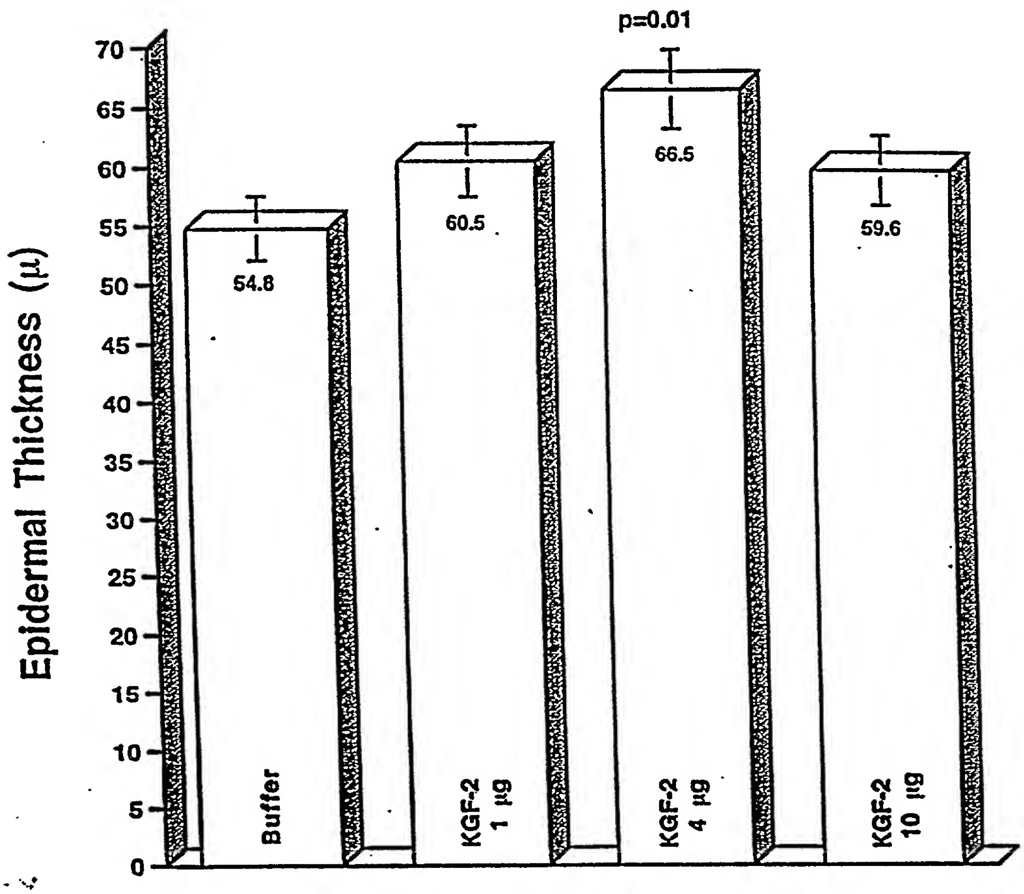
Treatment Groups	Wound Size (mm)	%Wound Closure	Histological Score	Re-epith. (μm)	BrdU Score
No Treatment	25.9 ± 2.5	58.8 ± 3.7	6.8 ± 0.2	1142 ± 141	3.8 ± 0.4
Buffer	25.1 ± 1.7	60.2 ± 2.6	6.4 ± 0.2	923 ± 61	5.0 ± 0.4
KGF-2/Δ33 (0.1μg)	22.0 ± 0.9	65 ± 1.4	6.8 ± 0.2	1275 ± 148	4.6 ± 0.7
KGF-2/Δ33 (0.4 μg)	21.1 ± 1.4	68.4 ± 2.4	8.0 ± 0.5 p=0.0445*	1310 ± 182	4.2 ± 0.7
KGF-2/Δ33 (1.0μg)	19.9 ± 1.5	66.2 ± 2.1	8.4 ± 0.4 p=0.0159* p=0.0053†	1389 ± 115 p=0.0074†	3.3 ± 0.25 p=0.0217†
KGF-2/Δ33 (4.0μg)	18.1 ± 1.6 p=0.0398* p=0.0200†	71.2 ± 2.6 p=0.0367* p=0.0217†	8.5 ± 0.3 p=0.0047* p=0.0445†	1220 ± 89 p=0.0254†	5.3 ± 0.9

Figure 38



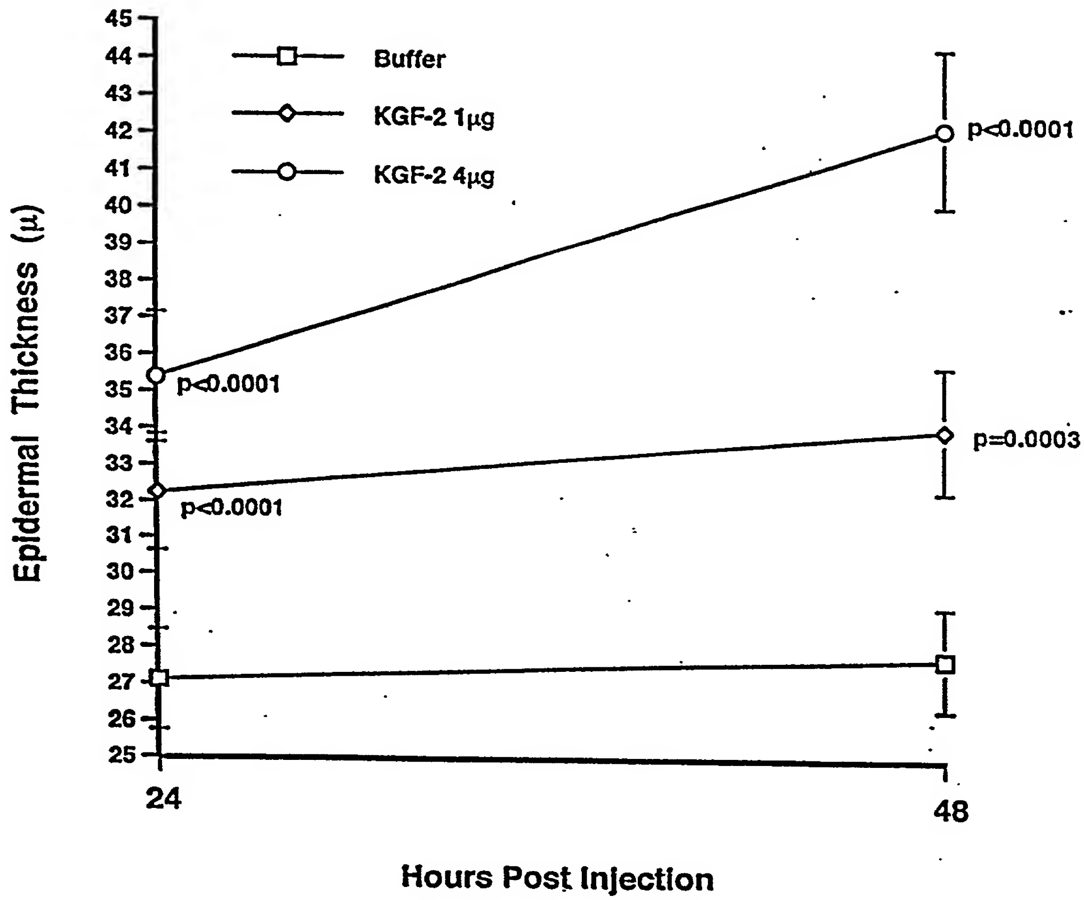
Breaking Strength (g)
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0
p=0.0006
p<0.0001
p<0.0001
44.5
107.3
126.4
123.8
Buffer
KGF-2 1 µg
KGF-2 4 µg
KGF-2 10 µg
n=8
n=8
n=9
n=8

Figure 39



Epidermal Thickness (μ)
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
p=0.01
54.8
60.5
66.5
59.6
Buffer
KGF-2 1 μg
KGF-2 4 μg
KGF-2 10 μg

Figure 40



Buffer
KGF-2 1µg
KGF-2 4µg
p<0.0001
p<0.0001
p<0.0001
p=0.0003
Epidermal Thickness (µ)
45
44
43
42
41
40
39
38
37
36
35
34
33
32
31
30
29
28
27
26
25
24
48
Hours Post Injection

Figure 41

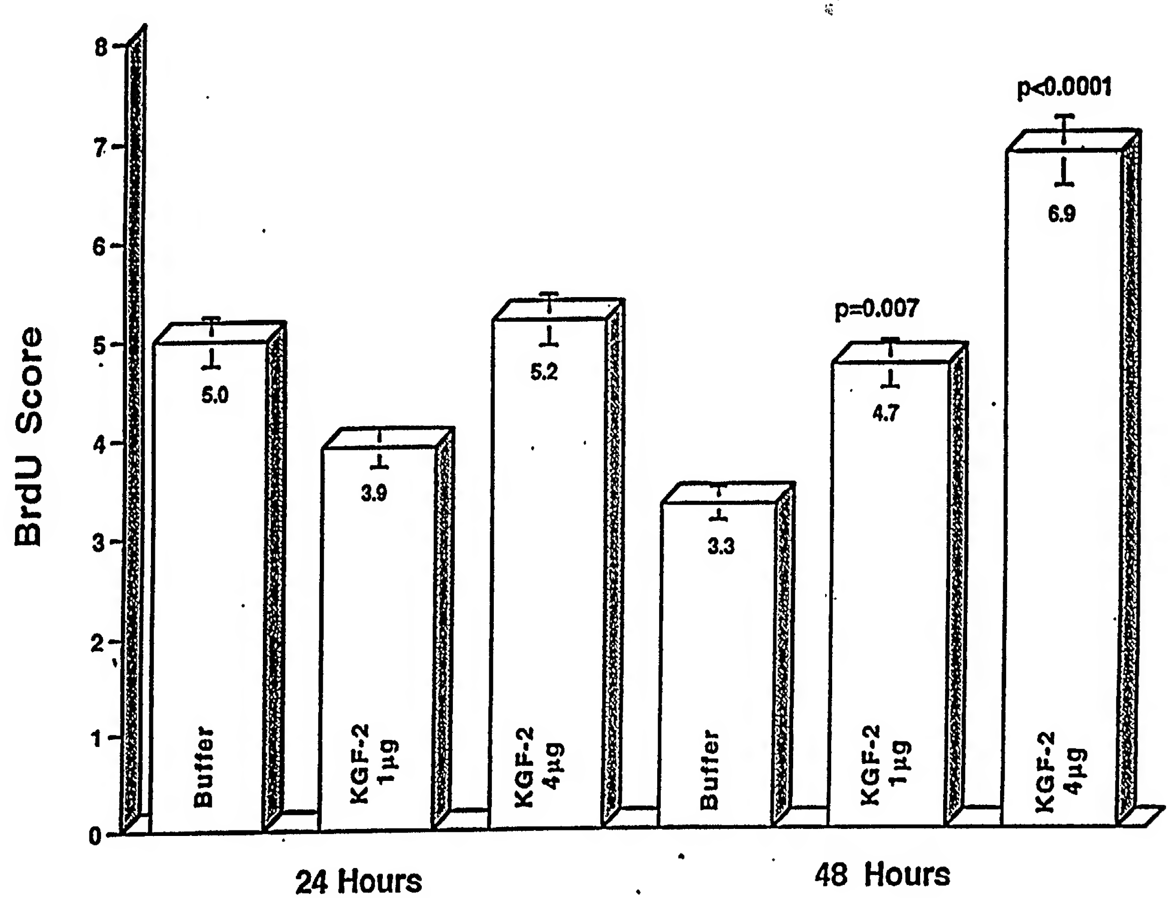
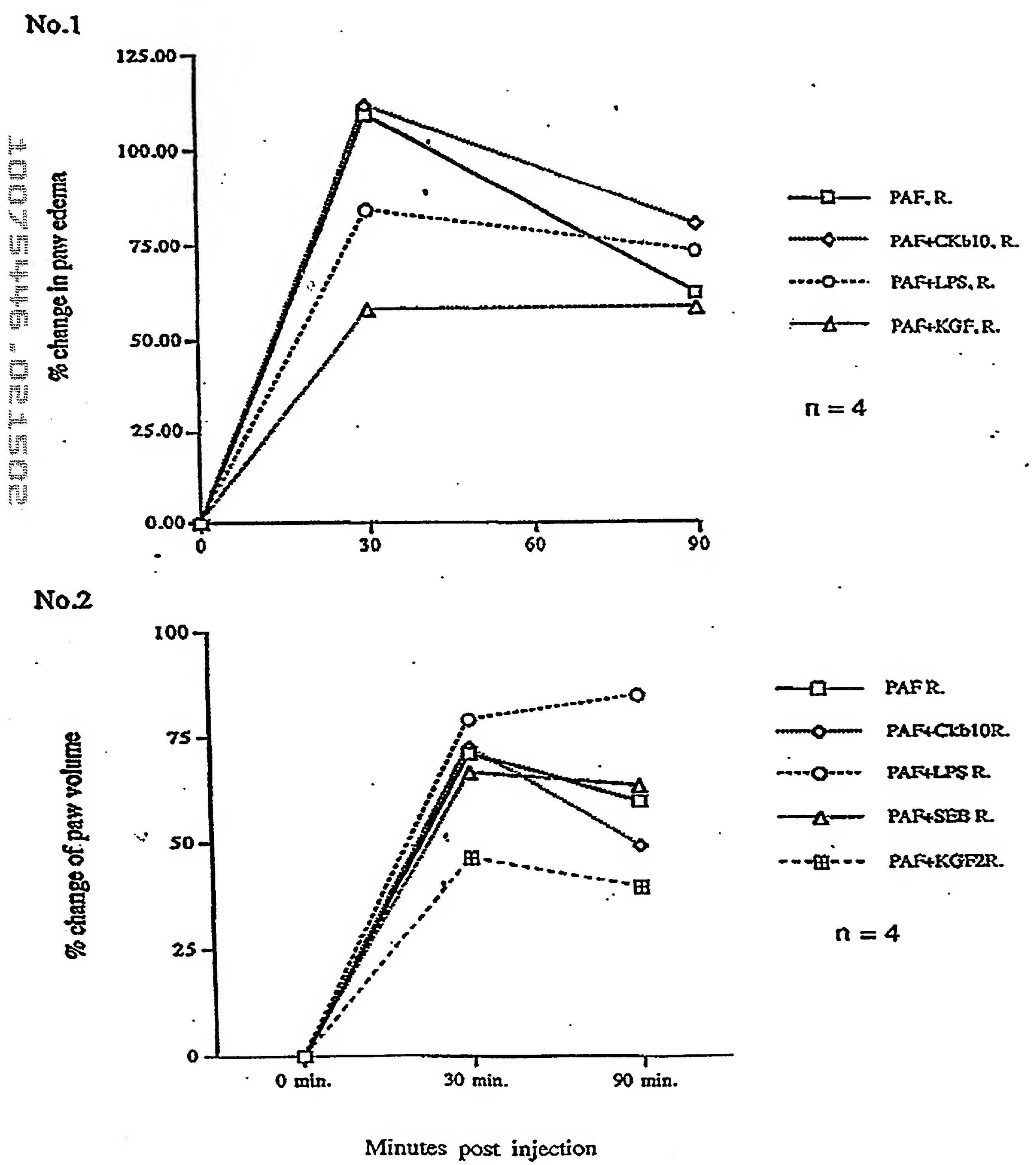

BrdU Score
8
7
6
5
4
3
2
1
0
5.0
3.9
5.2
3.3
p=0.007
4.7
p<0.0001
6.9
Buffer
KGF-2 1µg
KGF-2 4µg
Buffer
KGF-2 1µg
KGF-2 4µg
24 Hours
48 Hours

Figure 42



No.1
125.00
100.00
75.00
50.00
25.00
0.00
% change in paw edema
0
30
60
90
PAF. R.
PAF+CKb10. R.
PAF+LPS. R.
PAF+KGF. R.
n = 4
No.2
100
75
50
25
0
% change of paw volume
0 min.
30 min.
90 min.
PAF R.
PAF+Ckb10R.
PAF+LPS R.
PAF+SEB R.
PAF+KGF2R.
n = 4
Minutes post injection

Effect of KGF-2 Δ33 on PAF-induced paw edema in Lewis rats

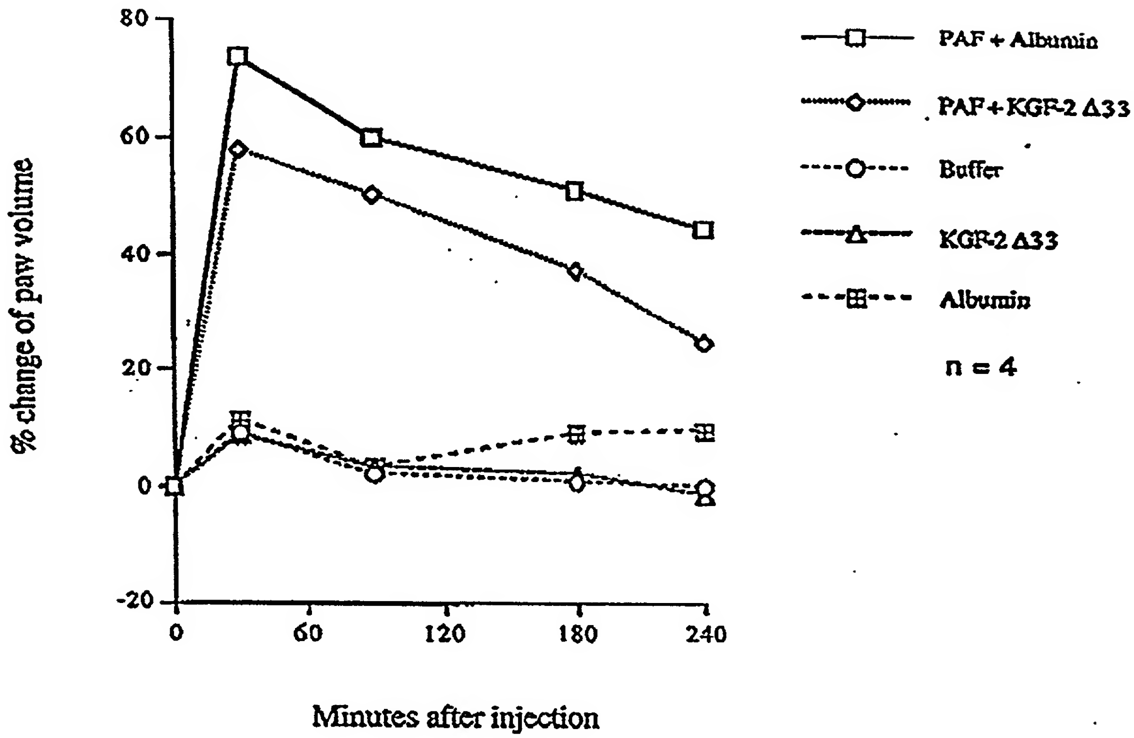


Figure 43

Effect of KGF-2 Δ33 on Survival of Whole Body Irradiated Balb/c Mice

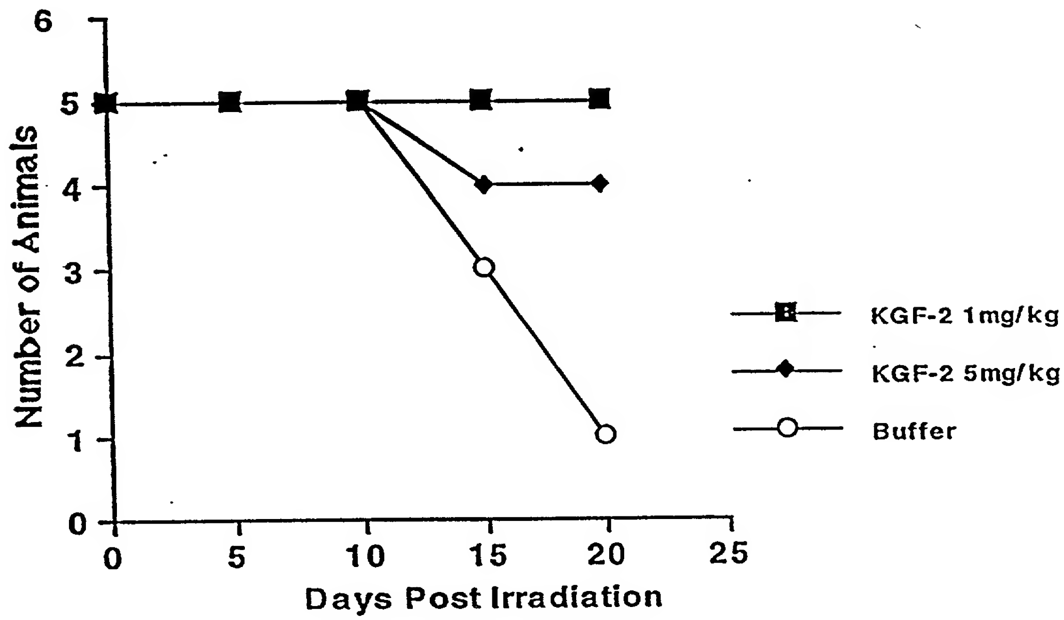


Figure 44

Effect of KGF-2 Δ33 on Body Weight of Irradiated Mice

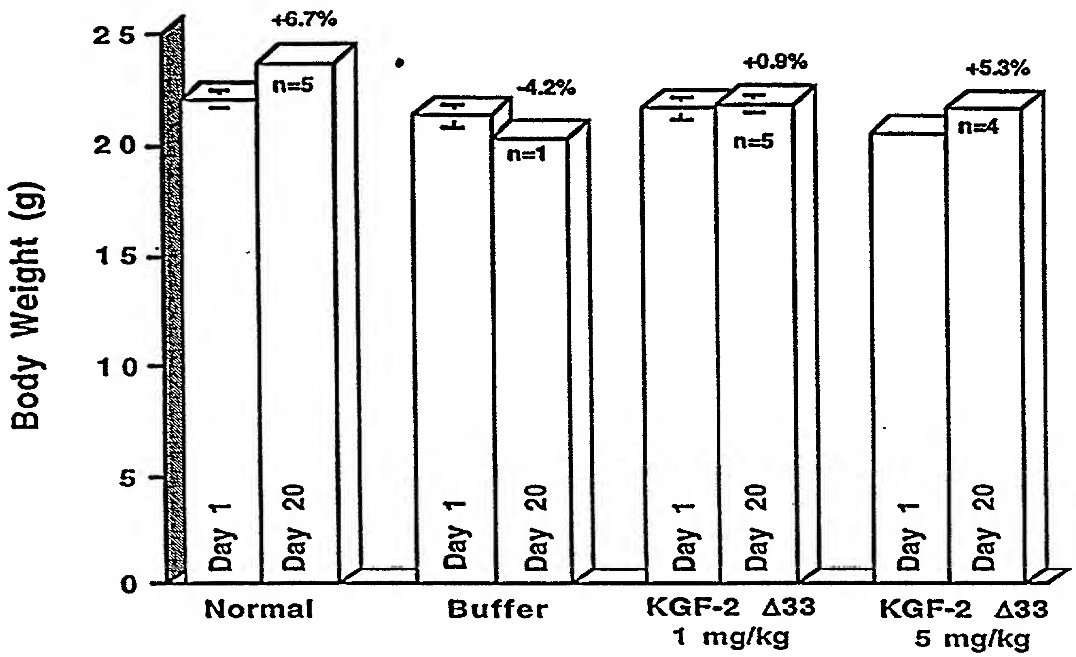
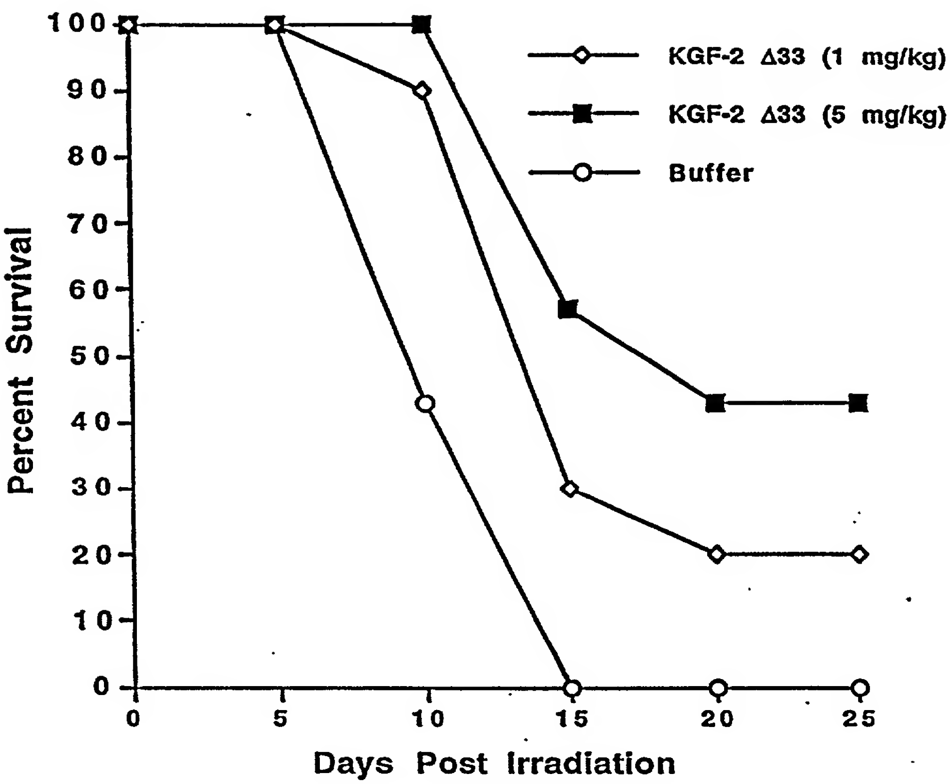


Figure 45



100
90
80
70
60
50
40
30
20
10
0
Percent Survival
0
5
10
15
20
25
Days Post Irradiation
KGF-2 Δ33 (1 mg/kg)
KGF-2 Δ33 (5 mg/kg)
Buffer

Figure 46

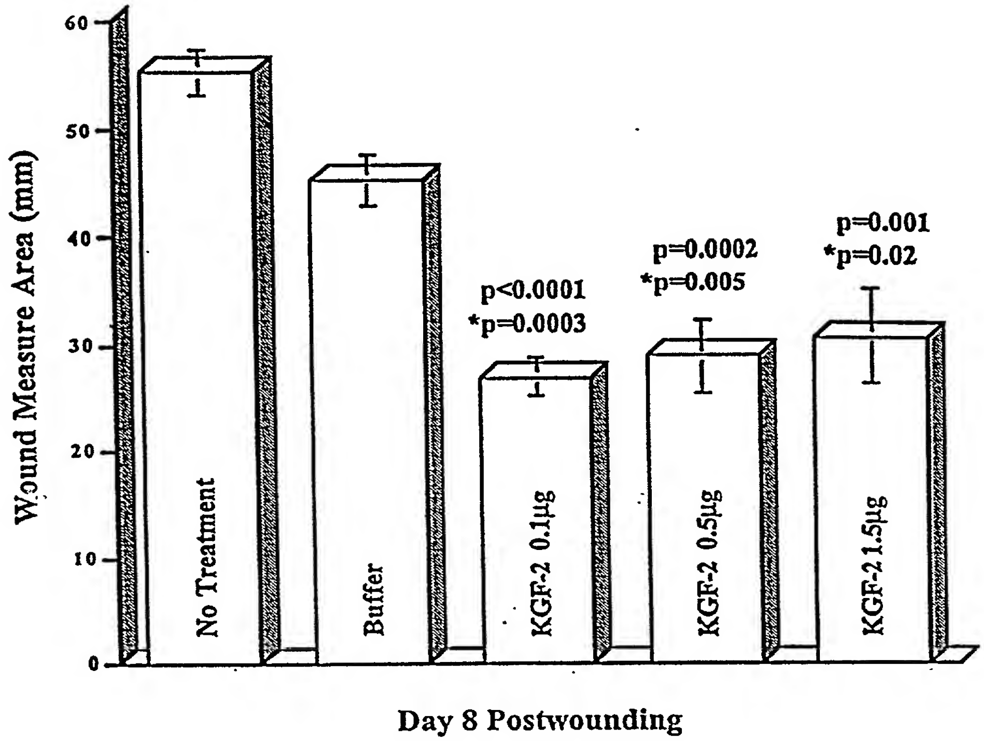
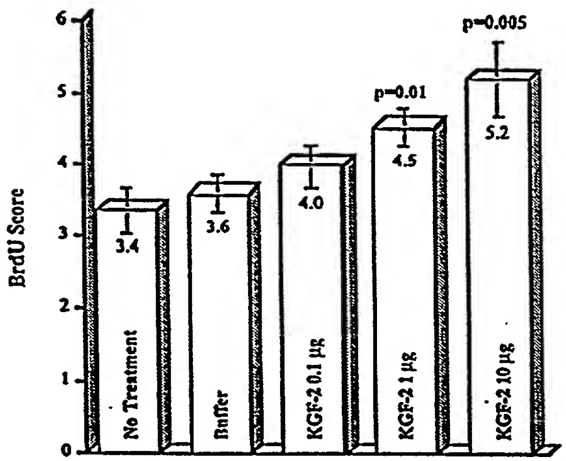
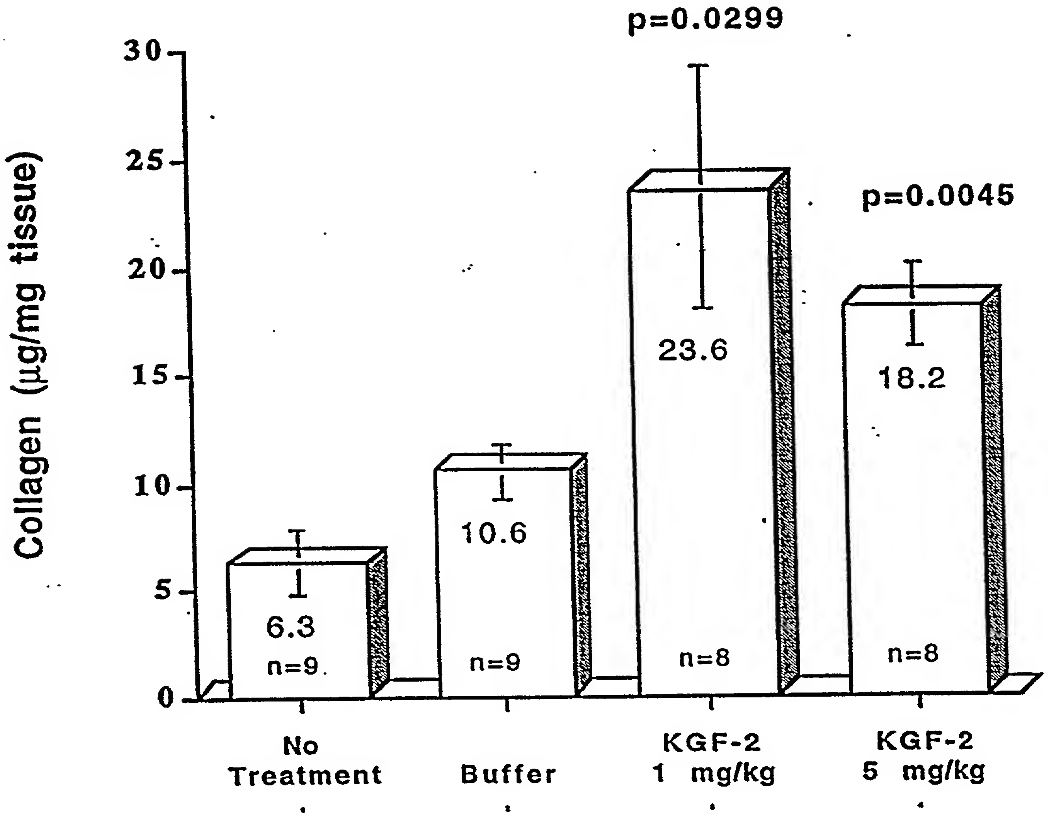

60
50
40
30
20
10
0
Wound Measure Area (mm)
No Treatment
Buffer
KGF-2 0.1µg
KGF-2 0.5µg
KGF-2 1.5µg
p<0.0001
*p=0.0003
p=0.0002
*p=0.005
p=0.001
*p=0.02
Day 8 Postwounding

Figure 47

Figure 48

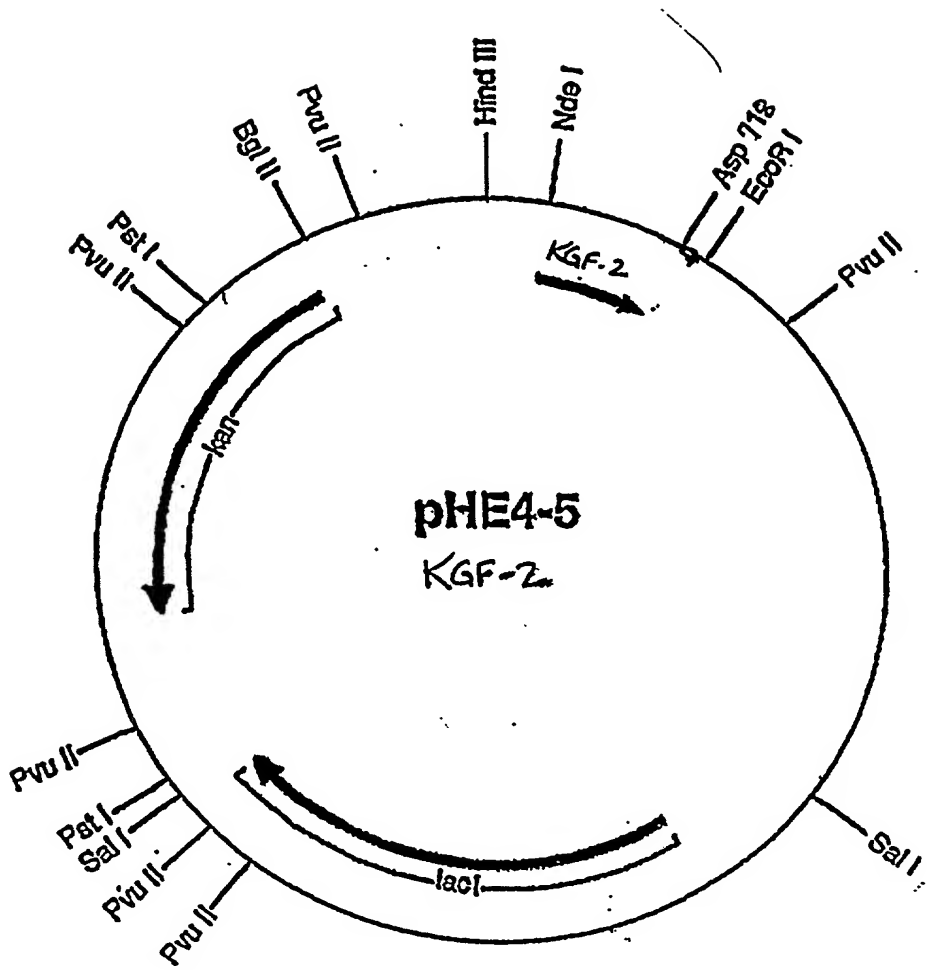


BrdU Score
6
5
4
3
2
1
0
p=0.01
p=0.005
3.4
3.6
4.0
4.5
5.2
No Treatment
Buffer
KGF-2 0.1 µg
KGF-2 1 µg
KGF-2 10 µg



p=0.0299
p=0.0045
Collagen (µg/mg tissue)
30
25
20
15
10
5
0
6.3
n=9
10.6
n=9
23.6
n=8
18.2
n=8
No Treatment
Buffer
KGF-2 1 mg/kg
KGF-2 5 mg/kg

Figure 49



Hind III
Nde I
Pvu II
Bgl II
Asp 718
EcoR I
Pst I
Pvu II
KGF-2
Pvu II
kan
pHE4-5
KGF-2
Pvu II
Pst I
Sal I
Pvu II
Pvu II
lacI
Sal I

FIGURE 50

FIGURE 51

-35 Operator 1
1 *AAGCTT* AAAAAACTGCAAAAAATAGT TTGACT TGTGAGCGGATAACAAT

-10 Operator 2
50 TAAGAT GTACCCA ATTGTGAGCGGATAACAAT TTCACACATTAA

S/D
94 A GAGGAG AAATTA *CATATG*

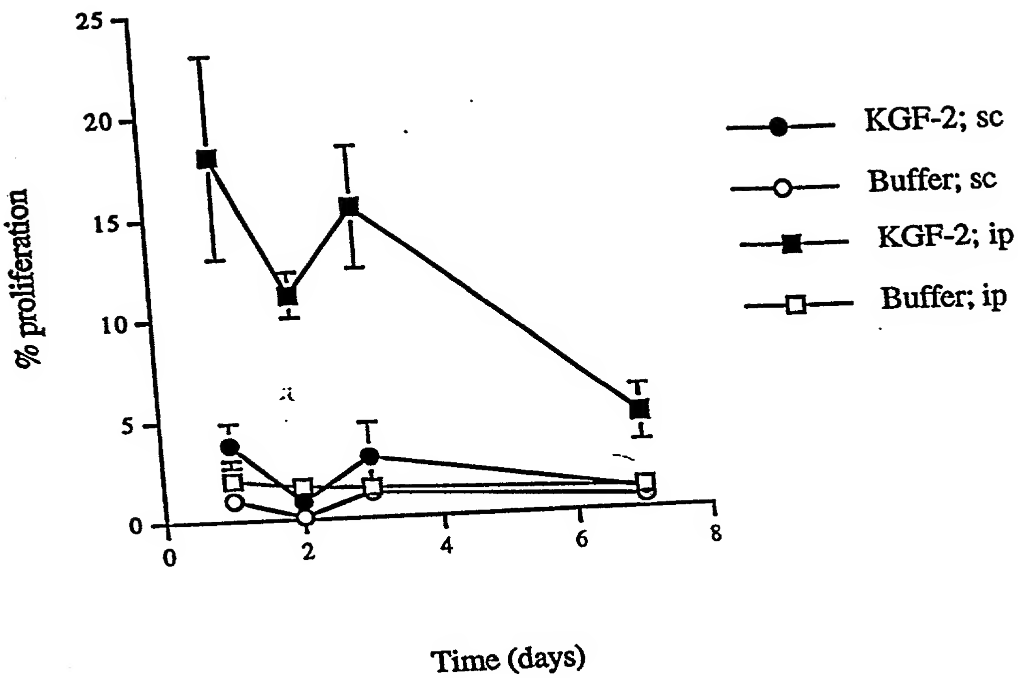
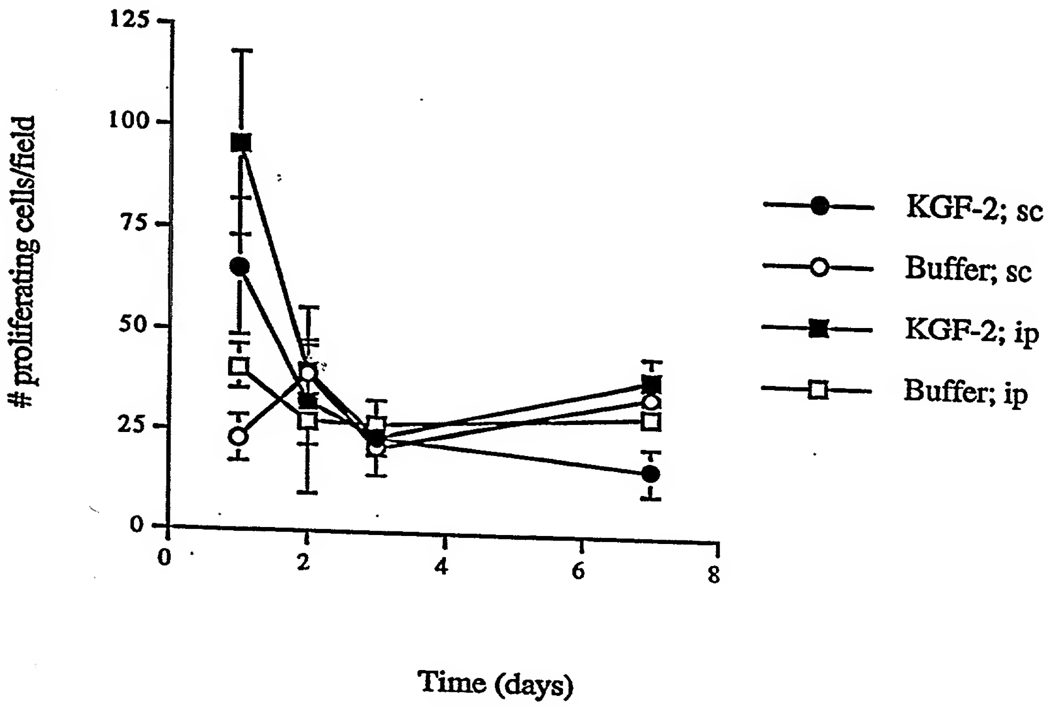

KGF-2; sc
Buffer; sc
KGF-2; ip
Buffer; ip
% proliferation
Time (days)
25
20
15
10
5
0
0
2
4
6
8

FIGURE 52



125
100
75
50
25
0
proliferating cells/field
0
2
4
6
8
Time (days)
KGF-2; sc
Buffer; sc
KGF-2; ip
Buffer; ip

FIGURE 53

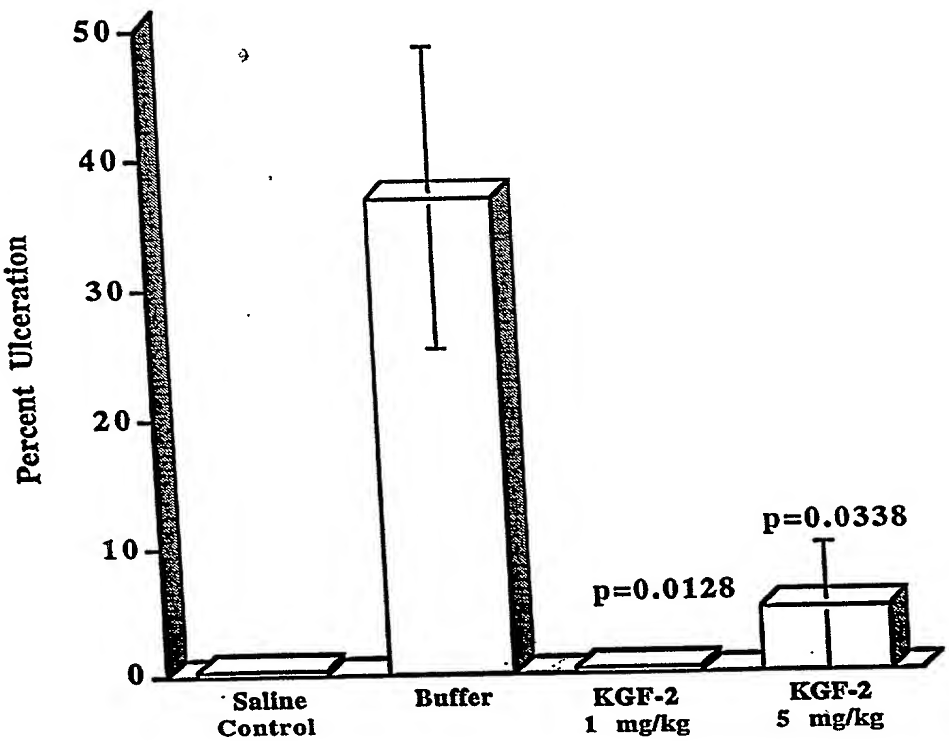

Percent Ulceration
50
40
30
20
10
0
p=0.0128
p=0.0338
Saline
Control
Buffer
KGF-2
1 mg/kg
KGF-2
5 mg/kg

FIGURE 54

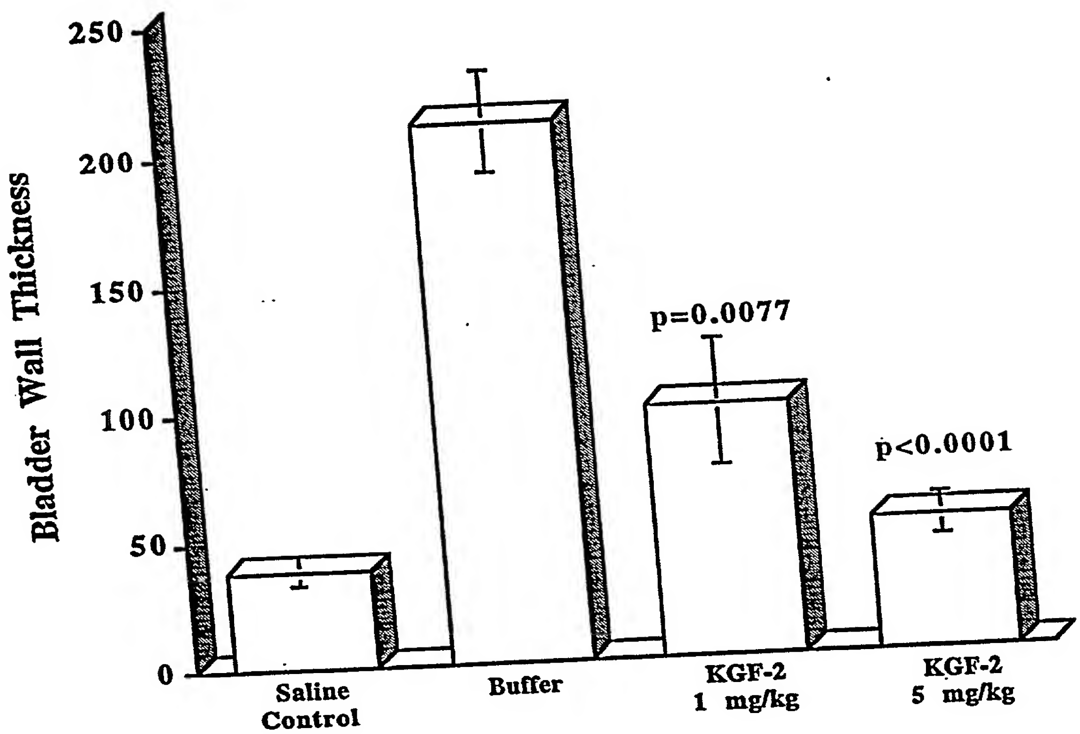

Bladder Wall Thickness
250
200
150
100
50
0
p=0.0077
p<0.0001
Saline Control
Buffer
KGF-2 1 mg/kg
KGF-2 5 mg/kg

FIGURE 55

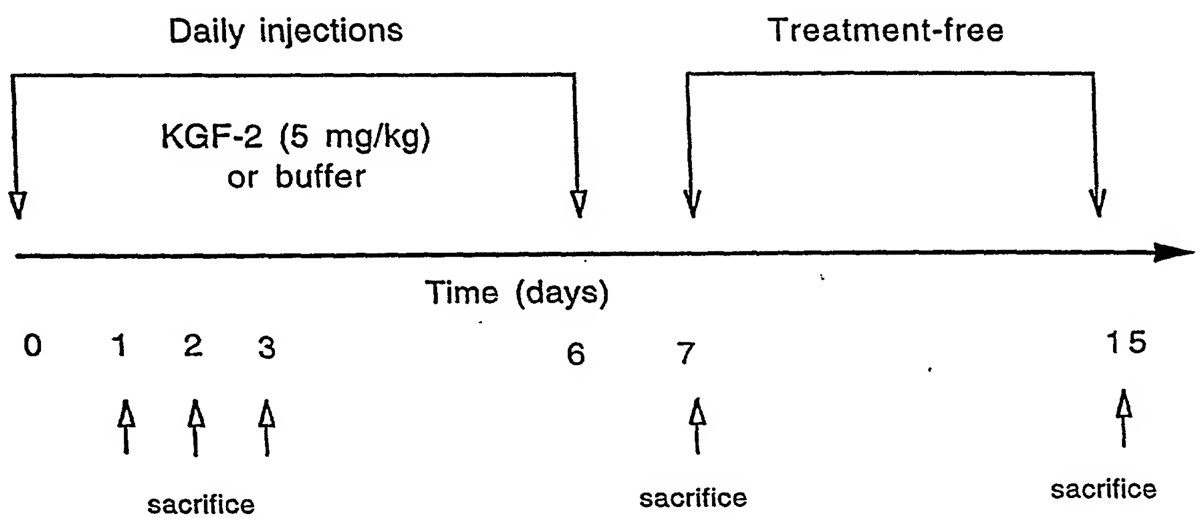

Daily injections
Treatment-free
KGF-2 (5 mg/kg)
or buffer
Time (days)
0
1
2
3
6
7
15
sacrifice
sacrifice
sacrifice

FIGURE 56

Proliferation of hepatocytes following systemic administration of KGF-2

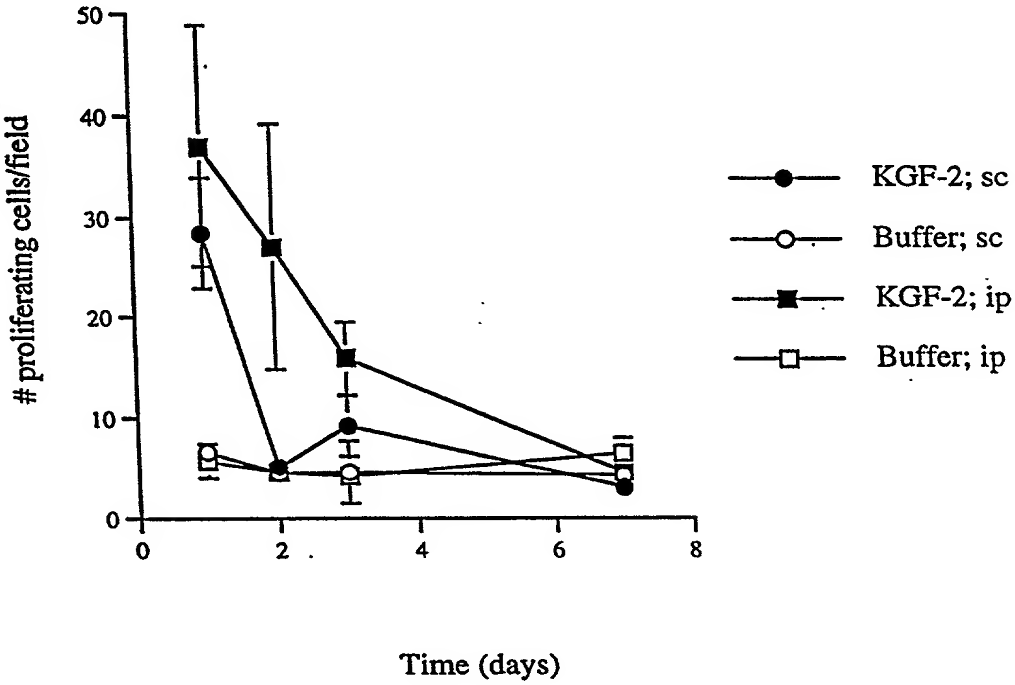


FIGURE 57

Proliferation of pancreatic cells following systemic administration of KGF-2

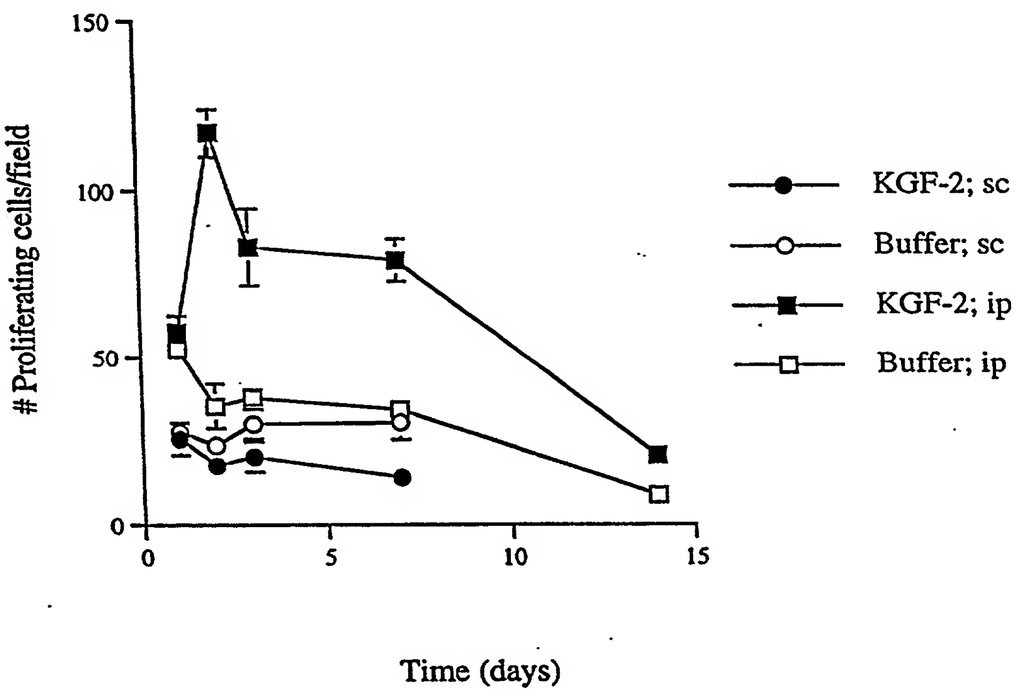


FIGURE 58

Proliferation of renal epithelia after systemic administration of KGF-2

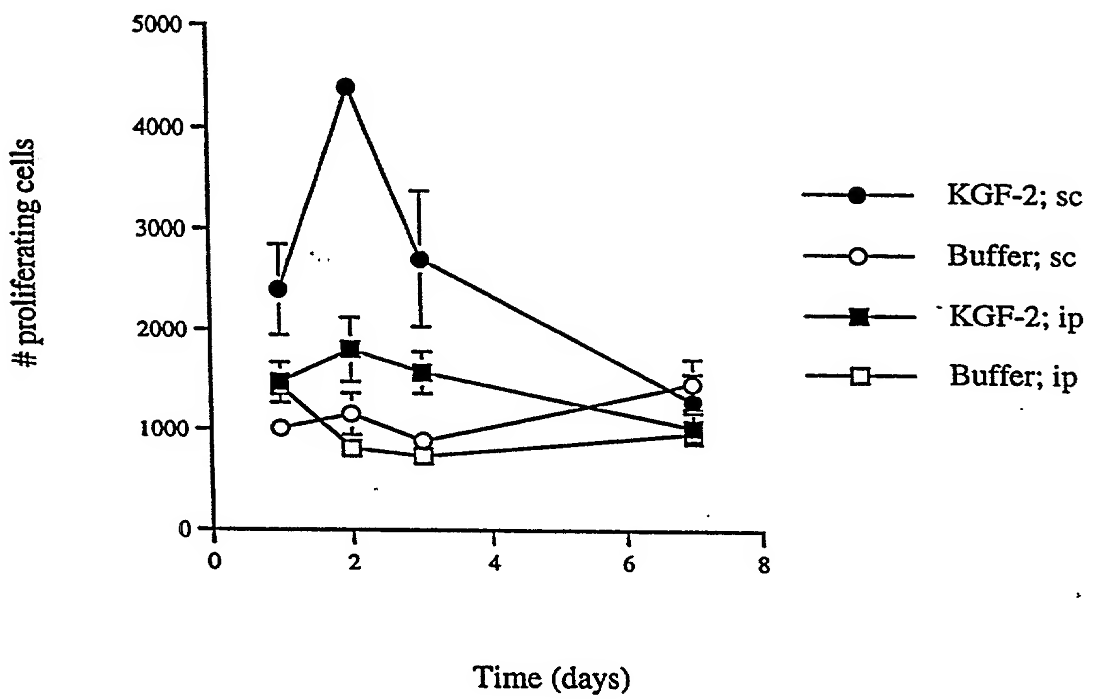
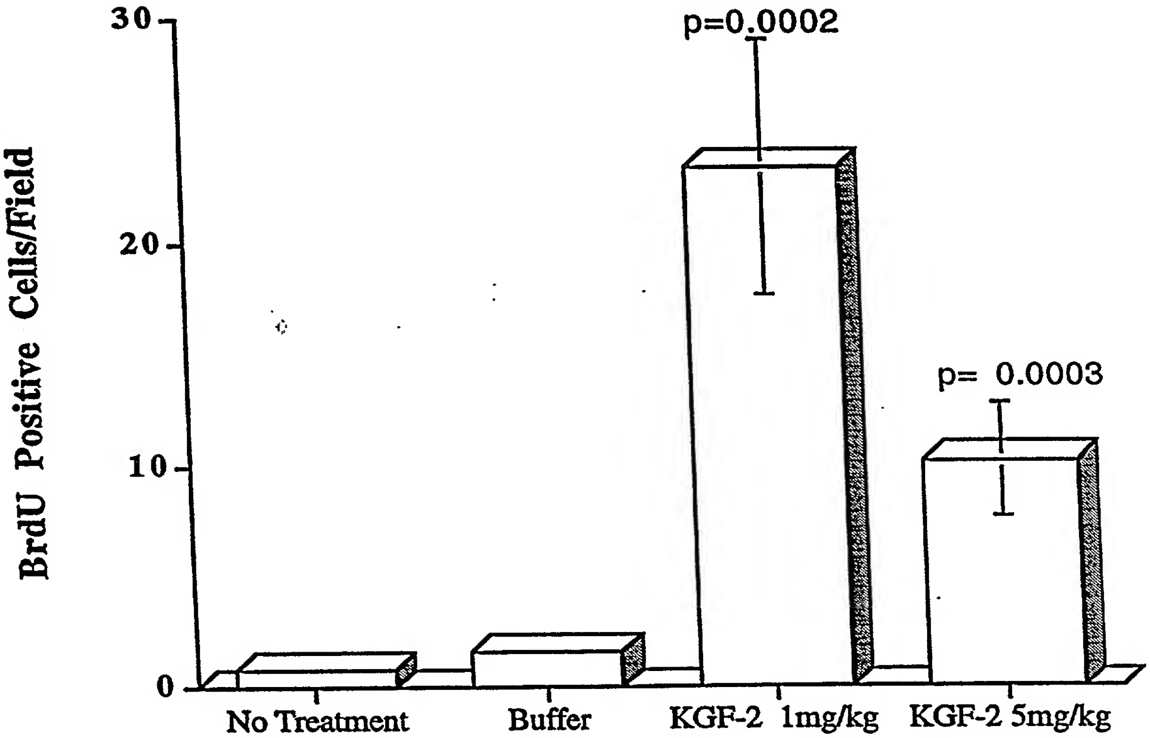


FIGURE 59



30
20
10
0
BrdU Positive Cells/Field
p=0.0002
p= 0.0003
No Treatment
Buffer
KGF-2 1mg/kg
KGF-2 5mg/kg

FIGURE 60